Supplementary Information to:

Comparative genome analysis of *Pseudomonas knackmussii* B13, the first bacterium known to degrade chloroaromatic compounds

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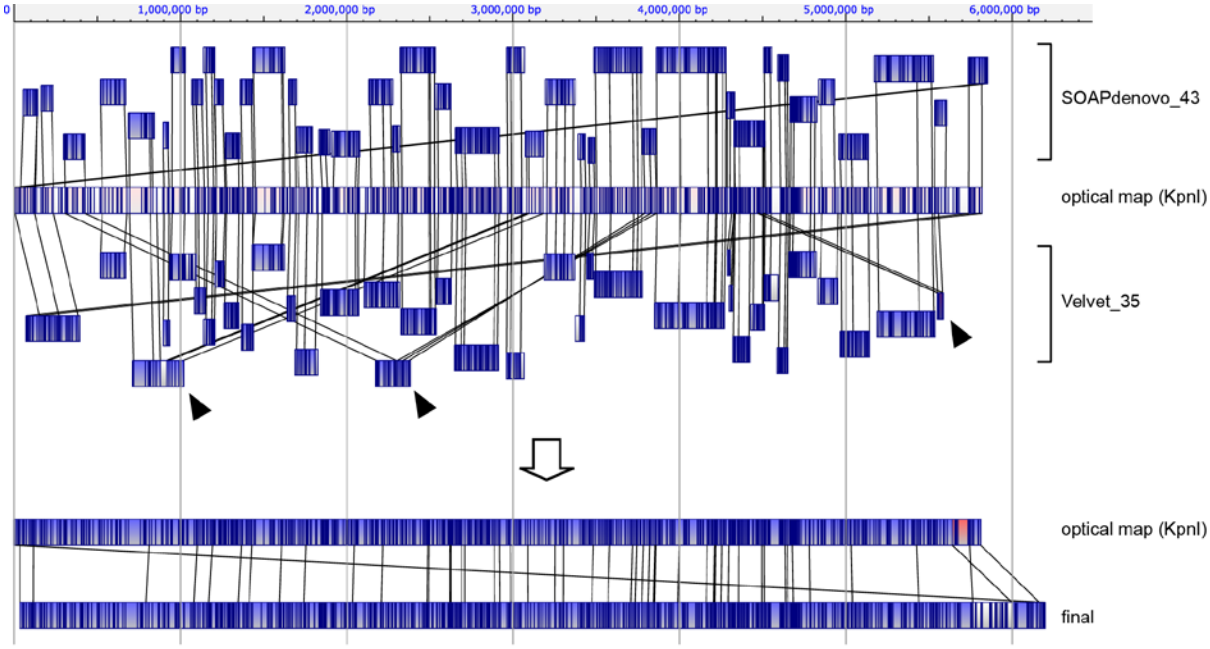

Fig. S1. Verification of the *de novo* assembly of the B13 genome by optical mapping. Contigs generated by SOAPdenovo (kmer = 43) or Velvet (kmer = 35) were aligned on the optical map (prepared for KpnI). Three misassembled contigs by Velvet are indicated by black arrowheads. The final B13 genome was verified for the same restriction enzyme with the optical map. Note how the two ICE*clc* copies are collapsed in the original map (red), but appear in duplicate on the final corrected optical map.

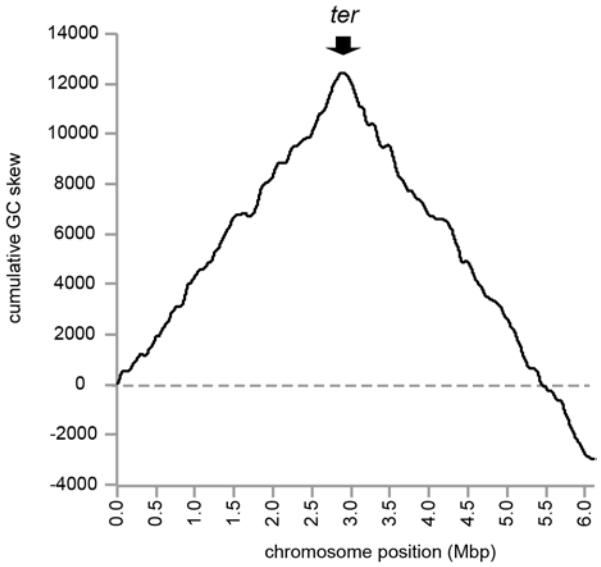

Fig. S2. Cumulative GC-skew plot of the B13 genome. The position +1 corresponds to the predicted origin of replication (*oriC*), whereas the predicted termination site of replication (ter) is indicated by an arrow. Note how the right replichore is longer than the left because of the presence of two ICE*clc* copies.

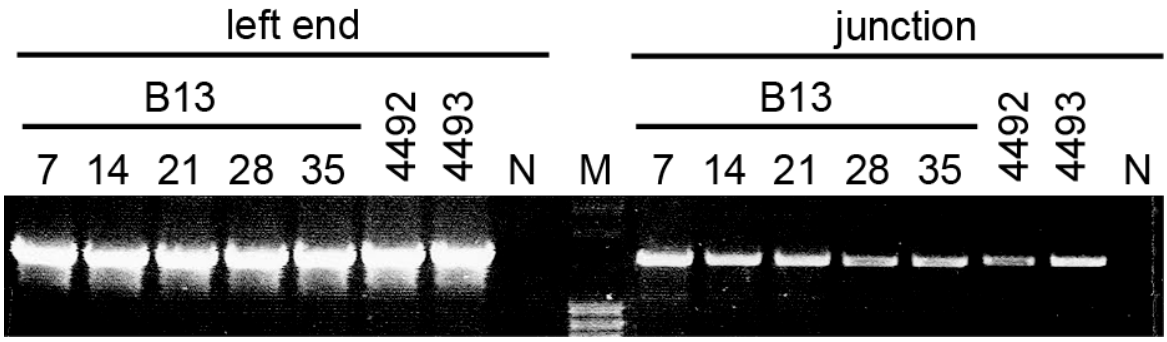

Fig. S3. PCR analysis of instability of USR1 in B13. DNA from B13 cultures in MM with 5 mM of 3CBA after 7, 14, 21, 28 and 35 generations was used in the PCR. Pictures show amplicons of the 1.6-kb left border of USR1 (between PKB_2522 and PKB_2524) and of the 1.5-kb junction between PKB_2522 and PKB_2737 formed by the loss of USR1. B13-4492 and B13-4493 are two mutants with single *parB* deletions. N, *P. putida* KT2440 culture used as negative control; M, Mass-ruler DNAladder (Fermentas). Note how all cultures except *P. putida* amplify both the left border (in high amounts) and the junction (in lower amounts), indicating that a small proportion of cells in culture lost USR1 through recombination.

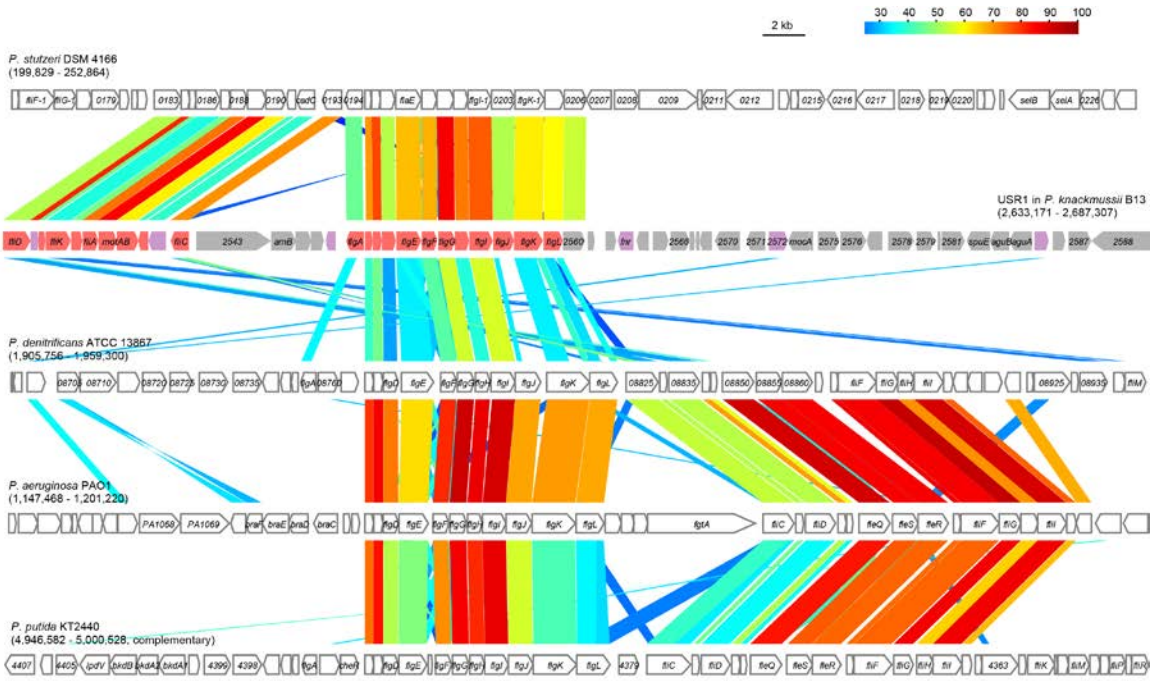

Fig. S4. Comparisons of flagellar associated genes in USR1 of B13 with orthologous genes in genomes of other Pseudomonads. Maps show relevant genome regions (coordinates displayed) with location of predicted genes as open or colored pentagons (indicating the direction of the gene). Colored bars linking genes show the percentage amino acid similarity calculated by Blastp comparison in GenomeMatcher, according to the color scale. Colors of genes in B13 region UMR1 refer to gene functions mentioned in Fig. 5.

Table S1. Assembly statistics of the genomes of *Pseudomonas knackmussii* B13 and its mutants.

B13	n	n:1000	n:N50	min	median	mean	N50	max	sum
CLC-Bio	245	210	39	1097	17920	28428	50763	159717	5970069
AbySS_37	170	148	27	1020	31083	45717	78309	279608	6766152
Velvet_35	99	73	11	1100	42111	82258	192483	421851	6004857
SOAPdenovo_43	142	93	14	1006	36177	64401	153908	421511	5989310
B13-2201									
CLC_Bio	270	179	35	1006	23147	32145	56790	159786	5753996
AbySS_57	225	124	23	1097	32949	50355	78344	239542	6244117
Velvet_51	163	92	11	1073	23724	63107	180491	424547	5805858
SOAPdenovo_47	290	98	16	1082	37035	58488	119747	349553	5731875
B13-2811									
CLC_Bio	789	454	77	1046	7826	12421	21768	118840	5639180
AbySS_27	240	138	24	1095	30424	46012	81356	221737	6349687
Velvet_27	164	83	11	1044	31609	69118	179406	458934	5736806
SOAPdenovo_25	391	101	18	1122	33849	56902	110871	250668	5747106

N = number of contigs

n :1000 = number of contigs > 1000bp

n :N50 = number of contigs > N50

min = smallest contig

max = largest contig

sum = sum of all nucleotides in the assembly (without Ns)

Table S2. In silico prediction of potential prophage regions in the B13 genome by PHAST.

CDS_POSITION	BLAST_HIT	B13 Gene Nr		EVALUE	prophage_PRO_SEQ
#### Prophage 1 ####					
612110..613603	PHAGE_Pandor_salinus: P-aminobenzoic acid synthase	PP_00578	phage(gi531034920)	9.00E-42	MNREAFQRLAAEGYNRIPLTCETLADFDTPLSIYLKLADGPNTYLLESVQGGEKWGRYSIIGLQCRTVLR
complement(613716..614039)	PHAGE_Burkho_AH2: excisionase	PP_00579	phage(gi399529070)	5.00E-05	MLPSSLDNPPAPRQETVTLVYQIFGDVLVPLEQVRERWFRNLNRENFGKALACGRIALPVTTLDDSHKAM
complement(614172..614942)	PHAGE_Pseudo_F116: transcriptional regulator	PP_00580	phage(gi56692918)	3.00E-54	MNSTPSPSTLAERLKQAMAARNLKQETLAEAAGVSQNTIHKLTSGKAQSTRKLIEIAAALGVSPIWLGTG
615344..615553	PHAGE_Vibrio_VP882: conjugative transfer protein	PP_00581	phage(gi126010902)	8.00E-11	MADLADYANDLMLERLDALIAARRHSAIPAAAEDCQVCGEPIPEARRQAVPGCDRCLDCQALEELERRR
615572..615931	hypothetical protein PA14_07980 [Pseudomonas aeruginosa UCBPP-PA14] gi|116054341|ref|YP_788786.1|	PP_00582		1.00E-46	VIKPIDEMLKLWAEEMHDPGVAGGGYAGGNLLAMMMANKGEMIRGTRGSRVLLDRVGELDLIVNGLPEQQ
615995..616489	acyltransferase [Cupriavidus taiwanensis LMG 19424] gi|194290122|ref|YP_002006029.1|	PP_00583		9.00E-43	MLAGMPSNTLFLQIRRATPADAEAILRVLGETYENTWKPQLAETARERFESAGRSGAYVAERLGDFHLAC
616774..617121	putative holin [Pseudomonas aeruginosa M18] gi|386056684|ref|YP_005973206.1|	PP_00584		5.00E-52	MGNEPQTLAEMPLWVLILLAALGGVSGEMWRADKAGLGGWVLLRRLALRSGASIVCGVAVMLLAMSCGAS
617154..617684	hypothetical protein PSPA7_0759 [Pseudomonas aeruginosa PA7] gi|152985833|ref|YP_001346154.1|	PP_00585		3.00E-42	MSEQPMTLDALLAAVEQTLAAQLTEIEQILRGPLGDIAPTPPALLLDLAQLQPDRDPGTGKTAVICALQA
617681..618244	PHAGE_Pseudo_phiCTX: predicted baseplate	PP_00586	phage(gi17313235)	4.00E-21	MSQVYVSAEQDRRLAALVLPCVVVAVDLAAARVRVQSGEWTSAWVRWHDQAAGQARHWRAPSIGEQGVLL
618348..618674	PHAGE_Salmon_RE_2010: baseplate wedge subunit	PP_00587	phage(gi418489710)	8.00E-16	MIGMDRRTGQPLSGLAHLKQSIEDILSTPLGSRRMRPEYGSRLRRMVDLPLTEGWKSAVQAEVAYALGRW
618671..619561	PHAGE_Salmon_RE_2010: baseplate assembly protein J	PP_00588	phage(gi418489711)	1.00E-91	MSVIDLSQLPAPEVVESLDFEALYQDLLAAFRAAMGEGWNAALESDPVLKLLELAAYRELLLRARINDAA
619554..620168	PHAGE_Salmon_RE_2010: tail protein I	PP_00589	phage(gi418489712)	3.00E-57	MSSRLLPSNATPLERALADVQSADLPVPLRELMDPQHCPLALLPYLAWAWSVDRWDPTWPEAVKRKAVLA
620159..621307	PHAGE_Salmon_RE_2010: tail fiber protein	PP_00590	phage(gi418489713)	1.00E-56	MAVTYYALLTTIGASKLANASALGTTLKITQLAVGDGGGTVPTPDASRTALVNEVRRAPLNQLSVDPANA
621510..622667	PROPHAGE_Xylell_Temecula1: contractile tail sheath protein	PP_00591	phage(gi28198986)	1.00E-85	MSFFHGVTVTNVDIGARTIALPSSSIIGLVDTFAPGASVSAQADVPVLITSLREAAAAFGVDSAIYKSCV
622680..623183	PHAGE_Vibrio_vB_VpaM_MAR: tail tube protein	PP_00592	phage(gi428782747)	6.00E-30	MIPQTLSNTNLFIDGVSFAGDVPSLSLPKLSVKTQDYQAGGMDAPIALDMGLEKMEAKFSTNGARREALN
623194..623505	hypothetical protein PSPA7_0767 [Pseudomonas aeruginosa PA7] gi|152983692|ref|YP_001346162.1|	PP_00593		2.00E-36	MTQAQPVWLSLGADAATVRLSRPAQCNGVSVDSLTLRAPTVRDIRLATRVGGDAEERELQLFASLAQVSA
623664..625631	PHAGE_Bacill_phiAGATE: putative tail lysin 2	PP_00594	phage(gi448260828)	1.00E-16	MSEQQKITVVLGGVLDASFGAVMADAKDRVEALRRDSERAFNLQGFVGETRRLQQEYLQLHRIGDAGASI
625697..626545	PHAGE_Vibrio_vB_VpaM_MAR: putative tail protein	PP_00595	phage(gi428782751)	8.00E-14	MAYTEQLQAALKSIGEAIESRHQDLSKKVSPVDAAIGELQAATAELEKQLGLPPDVSSALQRVMRGIDQA

626529..626738	PHAGE_Salmon_RE_2010: tail component protein	PP_00596	phage(gi418489702)	1.00E-09	MATICRTADGDCLDSLCQQHYGHLLGTLEATLDANPGLADEPQPLP AGLLIALPELPAAPSSPQVRLWD
626785..627813	PHAGE_Salmon_RE_2010: gene D protein	PP_00597	phage(gi418489726)	2.00E-41	VQPTFRLIADGNDITKLLSARLLSLTLSDKTGQTSDTLELVLDDRDGEI ELPRRGALLDVLLGYQGQELT
627827..628465	PHAGE_Pseudo_F10: Predicted chitinase	PP_00598	phage(gi148912826)	3.00E-43	MSITAEQLLQLFPKAAPLLPWLLPAMQARGVDTAIRQAAFLAQVG HESAGLTRWVESLAYSAQGLADTWP
628576..629148	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp021	PP_00599	phage(gi148912786)	7.00E-55	MQPALMPLNLIRGATYRDTRRFMQPRREYRDISAIAPSAPLRLTVP GHQLLGDWLVWVAGVSGFPELNRV
629156..629689	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp022	PP_00600	phage(gi148912787)	2.00E-09	MNDVEQTEPWAVAVEGDAPALVLEQINECAVTVSAGAELTVITVG EQGPPGPKGVPGPAGGSALQKVAAV
629693..630208	PHAGE_Roseop_EE36P1: hypothetical protein EE36P1_gp32	PP_00601	phage(gi237651492)	1.00E-35	MAGDKFLMNNNGNLQEVAATQISAGAASAGDIPALDASGRLDTS MMPVGLGADTAVVTASEALAAGDYVN
630213..631679	PHAGE_Entero_T5: L-shaped tail fiber protein	PP_00602	phage(gi46401894)	4.00E-23	MAQRRPLYSNGGTPAELPSGDTLAGAEPPITSGTAAQFWRGDKT WQDLGAAVRSAVLTGLSTAPAVSTAV
631743..632270	PHAGE_Thalas_BA3: hypothetical protein BA3_0023	PP_00603	phage(gi160700617)	9.00E-13	VMEWQAVLKTLAPWIGSAFGGPLGGLAVDAAASAMGLSDKTAEA VKQALSGATPEQLLAVKQADQAFALQ
632752..633348	PHAGE_Pandor_salinus: P-aminobenzoic acid synthase	PP_00604	phage(gi531034920)	5.00E-32	MLLMIDNYDSFTYNLVQYFAELKADIHVIRNDELSVDEIAALNPERI VLSPGPCTPNEAGVSLEVIERFS
#### Prophage 2 ####					
complement(773204..773572)	PHAGE_Pseudo_B3: transcriptional regulator	PP_00747	phage(gi56692569)	2.00E-40	MKIRSQQIRRRNNMLAELAELVVGSLKRHGIPVDKATAEAEELAFQ LHRRWAGITFAFPAKDDLARKRLE
complement(773569..774150)	PHAGE_Pseudo_B3: hypothetical protein B3ORF2	PP_00748	phage(gi56692570)	2.00E-74	MALAKALLSKIHIARQQLGLAEDVYRQKLQGMFGKASAKDLSQRQ AEKLLDEFKRLGWKPRPSSKSAGKP
complement(774150..774362)	PHAGE_Bacill_phBC6A51: hypothetical protein BC1874	PP_00749	phage(gi31415768)	8.00E-05	MKNKVEDLRNHLFATLEGLLDRDEPLDIERAKAVAQVGSVIIESAKV EVKAMELLNADRSKFLQIGEEPK
complement(774346..774882)	PHAGE_Bacill_phBC6A51: hypothetical protein BC1875	PP_00750	phage(gi31415769)	4.00E-24	MVYGKAKQLSLSKSAAFLEGPLSRRLDGSQGVQYRFAKGITPWNK GRKGSPSTGRMAETQFRPGNKPGNW
complement(775067..775468)	PHAGE_Pseudo_MP29: host nuclease inhibitor protein	PP_00751	phage(gi215479988)	1.00E-38	MTDTTVSVDTIMEQAQVFASAWSLVGGRFDQGDALEIAEEAKAEL REMLEDFCSNTELKRVAELLVTWHQ
complement(775470..776105)	PHAGE_Pseudo_B3: hypothetical protein B3ORF6	PP_00752	phage(gi56692574)	2.00E-41	MTEKQQTPSIHIPAGFVMNAAGHLVPEHQVREHDKLRDQVACDL VDEAVMLHNALASFKARALADIADLI
complement(776098..776577)	PHAGE_Pseudo_B3: hypothetical protein B3ORF8	PP_00753	phage(gi56692576)	8.00E-28	MNAPILNMHLADLLRQAQPYVGRAPSGPGQELSTKIVDALALIAP AEQYSAAGADVLAERRRQIHVEGFS
complement(776577..776864)	PHAGE_Pseudo_B3: hypothetical protein B3ORF9	PP_00754	phage(gi56692577)	6.00E-11	MNSAAPRVPIAPVHLAQLSDQEVRLLAEEAMVKLFRQDQKIYQLQ VNQNRLNQMLVKLLDLFIAENYAKL
complement(776861..777187)	PHAGE_Pseudo_B3: hypothetical protein B3ORF10	PP_00755	phage(gi56692578)	2.00E-20	MSTVQHIQPQQQPAAPALTYLTPEFAKHLGAFNAMTRALREAGIEI EALVEKDNRIFIRAEDSGLIKTNF
complement(777189..778382)	PHAGE_Pseudo_B3: putative transposase B subunit	PP_00756	phage(gi56692579)	1.00E-141	MQHLKEVLSTVKKNQRDLARAAEVSPATIAQIINHGHWPKSIDKAR LFGRIADFLYEHGANDGDIAALEE
complement(778382..780148)	PHAGE_Pseudo_B3: putative transposase A subunit	PP_00757	phage(gi56692580)	6.00E-163	MNPIHAQEILAAHQQALEAGAGGRTVIYRAAAERLGMSLATLYRKL ESLTMKDKPRKRRSDAGSTAIPLR
complement(780152..781078)	PHAGE_Pseudo_B3: hypothetical protein B3ORF13	PP_00758	phage(gi56692581)	5.00E-37	MARQPRTIDAPAEPEHLDQDALLEHQHQVARLTNEQDATVRAIAV QLGYQLPADCTDPDLIQRDIAANMR
complement(781130..781429)	PHAGE_Pseudo_B3: hypothetical protein	PP_00760	phage(gi56692582)	7.00E-23	MTRPTSSAARVLRVLKALRGHTLRGLSNTELAKALGESPANITRYM

	B3ORF14				DLLIEEGFATRYEDTGRFAPGIAF
complement(781426..781650)	hypothetical	PP_00759		N/A	MSPETLAQCMSVQEALEPFGGYTEGWNGPTQIKFSKRVMDLGKP LREVTVGELQDIAAAVAEEMKDYFYP
complement(781647..782066)	PHAGE_Pseudo_B3: hypothetical protein B3ORF15	PP_00761	phage(gi56692583)	9.00E-48	VDAARETRNRSADHLSFDYLALNNGSSLYKWQADGRLPLSLVLPLE HACGQPLITRYLAAAHGKLLVDIP
782247..782504	hypothetical	PP_00762		N/A	MSEHELRQEIAALREQYEIETAASRSAFVVLVRYLAEGQQLHIDELCT DLDAMCIARPEEQWQRSLMALA
complement(782515..782739)	PHAGE_Pseudo_B3: hypothetical protein B3ORF16	PP_00763	phage(gi56692584)	1.00E-13	MSQNSIEHIDLIPHPLDAWRVALDALIACAPGDATAIAWHLADATR QLPDNSIAVEQLLPEATRANGKRL
complement(782751..782987)	hypothetical protein [Pasteurella multocida subsp. multocida str. 3480] gi|386834878|ref|YP_006240195.1|	PP_00764		2.00E-14	MKGNRKSPSAAPLPYPQTPTSANEWFIRHGVCKTHWARDMGLD RMVVVDLLRGRLKGLRGHAHEAAVALG
complement(783014..783418)	hypothetical	PP_00765		N/A	MNPAIQRLQDLLDQELQNAIACDRPVDYRQVFLGQLGQATLSDSD WIALSLSLLLAMSRGVAASDTSSAP
783679..783939	phage-related DNA-binding protein [Pectobacterium atrosepticum SCRI1043] gi|50122629|ref|YP_051796.1|	PP_00766		1.00E-08	VDVLYVVAGRRAELRSNATLPVAGDINTERLARIVEMLETFARSAGK RWPSAQLVAVAAEVYNVLLDEPA
784741..785238	PHAGE_Pseudo_B3: hypothetical protein B3ORF22	PP_00767	phage(gi56692590)	5.00E-08	MNKDVRIAAALLLAGFSVAGCSTKNYGRQPELTSFEQQTMSCREID LEQAKVQGFLAHVREESEFDGRSV
785910..786203	PHAGE_Pseudo_B3: holin	PP_00768	phage(gi56692592)	1.00E-38	MPSQQSRRRAPRMTSWTLVTLILLIVLAAIRPEQLQVVAYKLLLVTL GAVAGYWIDRTLFLVEARPHQCP
786260..786892	PHAGE_Pseudo_B3: endolysin	PP_00769	phage(gi56692593)	1.00E-93	LYALVAIFLMVWSLLHGAPACAQDRIPAQAEQYHRTLVRAAQAEW GLSAPIATFAGQIHQESRWRADARS
786991..787125	hypothetical	PP_00770		N/A	MLKDALRIVALSVALYALGLTFGKGLATGFSQNIQVNVRLQVAE
787122..787325	PHAGE_Pseudo_B3: hypothetical protein B3ORF26	PP_00771	phage(gi56692594)	5.00E-13	MTRLYLGCLMAQALTSVAMVAASANFLTAKELYCSPVPRERHGKSG VAKAKRKARQYKRRRAHHGRA
787312..787917	PHAGE_Pseudo_B3: putative Rz lysis protein	PP_00772	phage(gi56692595)	2.00E-71	MAVLSYLRAGWPILVVGLLALAMIVNSQAAYDNGFRKAKADGDA ALAQLREQYANERAQAAQDNLVQYKQ
787921..788310	PHAGE_Pseudo_B3: hypothetical protein B3ORF28	PP_00773	phage(gi56692596)	2.00E-61	MKIELELWQLISLLLAFLGGCAGGGKLLLNQIQKHLDARFASQDQA RLANHEQLSYRLGAIEQAAREETN
788300..788608	PHAGE_Pseudo_B3: hypothetical protein B3ORF29	PP_00774	phage(gi56692597)	7.00E-49	MQTDIAKIRRESLRWLILLTLNNARPVGSYEMPILSVAQSEYPDATP LEIRRELDYLSDRDLVKLDKQPS
788614..789186	PHAGE_Pseudo_B3: small terminase subunit	PP_00775	phage(gi56692598)	7.00E-91	MGRKSSISRLPDNVRAYIEGKLAEGRLTLDELIANLQAQFPSQAESG ELPSRTAVHRYGQKLERRLAAIR
789186..790640	PHAGE_Pseudo_B3: large terminase subunit	PP_00776	phage(gi56692599)	0	MKLKGNAKIIPANPEAIFLPYQSRWITDSSRLKLMQKSRQIGLSWST AYAADERTAAEDARVDQWVSSRD
790640..792112	PHAGE_Pseudo_B3: portal protein	PP_00777	phage(gi56692600)	0	MQQPKLGQEIATTGDGRDITRPFLSGLQQPSDYILQRRGGNDLRIY EEVLRDGQVKATWGQRQLAVVSRE
792112..793362	PHAGE_Pseudo_B3: hypothetical protein B3ORF33	PP_00778	phage(gi56692601)	1.00E-149	MATAASYGSLAFKEQIAFFEAKNPSVNYATVRGAAHDQSFVSAGA HRADLVADLFAVVNQAIRDGLTLEE
793359..793931	PHAGE_Pseudo_B3: hypothetical protein B3ORF35	PP_00779	phage(gi56692603)	1.00E-64	MSGARIEFEFDHQQVTQALNAGAAALGEPEKILQDLIDPLIRIHQA RFKAQQSPDGTPWQALSPRYLTSK
794147..795382	PHAGE_Pseudo_B3: protease	PP_00780	phage(gi56692604)	3.00E-179	MNKPTATLPILPAGSHVALDGRPVEFTEAALREIAETYNPALHEAPL VIGHPKLNAPAYGWAKSLEVRDG
795386..795766	PHAGE_Pseudo_B3: hypothetical protein	PP_00781	phage(gi56692606)	8.00E-48	MNIPGLTTAKRAVGAVAPRRICVHGASDGLAAQAADGTALLIGIST

	B3ORF37				DIPANDGQSFDVYRSGLAPVEYGG
795778..796710	PHAGE_Pseudo_B3: capsid protein	PP_00782	phage(gi56692607)	4.00E-152	MSNAPFPIDPELTAIAIAYRNGRMIADDVLPRVPVGKQEFKYWKYD LADGFTVPNTLVGRKSKPNEVEFD
796755..797426	PHAGE_Pseudo_B3: hypothetical protein B3ORF39	PP_00783	phage(gi56692608)	2.00E-43	MPRKTSTTKAEGQAAPAASIESKLPPEQQQATALQYIEGRLAGVQL HDGTVVPLAELPEADLRKIAMDME
797426..797779	PHAGE_Vibrio_VP882: p26	PP_00784	phage(gi126010879)	1.00E-44	MDNQHRKIAGYRELSPEEVDLMNRIKAKGAELLALQAELAGRLST DLETKRSNAIRSVAGKEFNGTPYNE
797790..798296	PHAGE_Pseudo_B3: hypothetical protein B3ORF40	PP_00785	phage(gi56692609)	3.00E-62	MYITLSELADRPGPEELSQAATPRRFRAVDADLLDALLRGNPVSDW TSEEVEIGTQALDVIVSAVNDAQA
798298..798753	PHAGE_Pseudo_B3: hypothetical protein B3ORF41	PP_00786	phage(gi56692610)	7.00E-57	MSSAPFDHNLVIDRLKDQVPELQDVGGAADLAAVTKIRDFRTPSAY VILAVETPIPRQSGAPGAATRQMV
798750..798962	PHAGE_Pseudo_B3: hypothetical protein B3ORF42	PP_00787	phage(gi56692611)	2.00E-13	MTTPIKKSQAAQAADEQQLEKVTLIAPHKHAGAKYQAGDEIEVNA IEKSFLLQHKKIAGASQEAAPAAKE
798966..799724	PHAGE_Pseudo_B3: hypothetical protein B3ORF43	PP_00788	phage(gi56692612)	1.00E-108	MSKLFSFQGKVFAGDRLANGTLSRPVWAGNVPAMSLKLSTDSTNK TESFSGKRLQYGRLQKGTTAQLDIT
799796..800239	PHAGE_Pseudo_B3: hypothetical protein B3ORF44	PP_00789	phage(gi56692613)	7.00E-43	VLHPERSLSIAGREITVREYGFVEGLGLRPLIQPFLDDLYALVNGRKGL PPLEEILGVLGKHSDLVAQLM
800467..804663	PHAGE_Pseudo_B3: tail length tape measure protein	PP_00790	phage(gi56692618)	2.00E-128	MAGKELDLALRIRADLADGQKALEGLGQSVVDVGDSAQQTNTRL AETGRAVDSLQADSAAAATALVAIDN
804660..805859	PHAGE_Pseudo_B3: hypothetical protein B3ORF52	PP_00791	phage(gi56692621)	1.00E-81	MSFVTGATPIWPVPPDWADGVRETLDWLTNYLPARNGRAQKREL RQAPRRSIEFTVISDEQGRRVADAIL
805849..806667	PHAGE_Pseudo_MP1412: tail assembly structural protein	PP_00792	phage(gi399529035)	2.00E-39	MTSESRESSWDQGKPVAFFRFTRKTRNWFYTSSDRDEVLLGDTYL RASISRTAIRQGSERARLNITITLP
806678..806899	PHAGE_Pseudo_B3: hypothetical protein B3ORF54	PP_00793	phage(gi56692623)	2.00E-10	MWVQIAILVVSALINYATRSKPTKPEPQEVTTPTAEEGKKLRKVYGT VWVDDAQVLGFKKMGTDPIQTKG
806896..807108	PHAGE_Pseudo_B3: hypothetical protein B3ORF55	PP_00794	phage(gi56692624)	2.00E-15	VIVTLAHLRSIPGYGPKPGFCASGSRAFFKRHGLDWDTFRREGIAAE ELAGTGDALAIALVEWARKVESA
807105..811862	PHAGE_Pseudo_B3: hypothetical protein B3ORF56	PP_00795	phage(gi56692625)	4.00E-99	MSSGSKKQTVGYWYRILGHYGLSKGPVDAFLELRGGDRTAWKGLL QASGRIHVAAKNLWGGKKSEGGLEG
811869..813326	PHAGE_Ectoca_siliculosus_virus_1: EsV-1-65	PP_00796	phage(gi13242537)	2.00E-32	MIFGNPFPYVKCLGDPIYRAERGEISRGATAFLLGGTINTLMVLGFLP NVFLTMYASQIGSALEVGLLSL
#### Prophage 3 ####					
1319317..1319328	attL			N/A	tggccgtaagca
complement(1319378..1320379)	PHAGE_Burkho_phiE125: putative site-specific integrase	PP_01269	phage(gi17975195)	2.00E-25	VGILMRPRKKDRHLPAKVYQKHGAFYYVHQGKWERLGSTLEAALK EYAKKVAPRSGGAMPDLIDEVLRHI
complement(1320645..1320767)	hypothetical	PP_01270		N/A	MRNALLYAGSAIALVFAVIGFCIIVPVIPAFMYWEWGCHL
complement(1320760..1321080)	hypothetical	PP_01271		N/A	MSINTQELATALNIVDGWLMSAECTIRITECRKCVTGARSALAKAIK GLQLRLPKSEAGGPLYSEGICDD
complement(1321077..1322126)	hypothetical	PP_01272		N/A	MTPRIPARRVAAQDQGCALAPATLSTKAPAARKRGGGLARRCLLTL SLAGRPSMPEGGAIESLCCAAAGI
complement(1322123..1322665)	PHAGE_Rhizob_16_3: p048	PP_01273	phage(gi195546578)	2.00E-26	MSWILTRTGRRFDLLEPAAHMIEPADIAHSLGRQCRFNGHTLTHYS VAQHCYIVADLVPVEHQLAALLHD
complement(1322662..1323336)	hypothetical protein Pmen_3990 [Pseudomonas mendocina ymp]	PP_01274		4.00E-35	MEFTTTQIIATAIILAFIAIVAGIAYWSGHRAGKETGYSEGRTTATNY WRPLIATKIAQRDEAQRLLDCR

	gi|146309004|ref|YP_001189469.1|				
complement(1323403..1323720)	hypothetical protein Psefu_0586 [Pseudomonas fulva 12-X] gi|333898787|ref|YP_004472660.1|	PP_01275		3.00E-18	MSQPDQQQLRLPVQARQATVELLFRTFGTVLIPLEDLRARYFRNLN SERFERVIGTERLPIPVTTLDGST
complement(1323717..1324169)	hypothetical protein Pmen_3987 [Pseudomonas mendocina ymp] gi|146309001|ref|YP_001189466.1|	PP_01276		7.00E-16	MKDIKLLDETLISLLRMPEDQRTAEVIKSHLTLASVAAGLKPEGLTDL QLEQMQLASAAALLAGQLGESF
complement(1324173..1324376)	hypothetical	PP_01277		N/A	MSHKPFLVIDGVALFPRRPREYVAAILQLKTLEERRAALAECPEEWQ DLIRTQLVIAWDHPQRNKAG
complement(1324366..1324659)	hypothetical protein PSPTO_3423 [Pseudomonas syringae pv. tomato str. DC3000] gi|28870587|ref|NP_793206.1|	PP_01278		5.00E-25	MKDLTLQETAKQLKTTRPKLIALMREKGLLNDQNLPAHPVRDRLYL SIHEGSWMHDKLGMQYSRSTRVRQ
complement(1324668..1325258)	hypothetical protein Pmen_3985 [Pseudomonas mendocina ymp] gi|146308999|ref|YP_001189464.1|	PP_01279		5.00E-40	MSQVFTLSDQSLALMTEQLNFSGAFNHTCRSAYSRHQIQLKMKVE RAVAETAVTIIMGGEKHSITLTTGA
complement(1325513..1326262)	PHAGE_Bordet_BPP_1: repressor protein cI	PP_01280	phage(gi41179362)	3.00E-24	LNSNKGVCSFVSMNTPTERQAVIAALFRKRREELKLSQSEVAKGVR ELLGGEVFTQQSYAAIEKGKTKHS
1326905..1327414	PHAGE_Burkho_phiE125: hypothetical protein phiE125p56	PP_01281	phage(gi17975217)	7.00E-10	MGRARFGQTERARRTLLTLPQALYHAAHDYPGGATALAAIDGTSAI TLSHKLSLTNTTHTPNIRDLDLIL
1327407..1327616	PHAGE_Pseudo_vB_PaeS_PMG1: DksA-like zinc finger domain containing protein	PP_01282	phage(gi374531723)	7.00E-06	MADIADIANDHVLQQQEQRLAARKPAVVEISEECHQCGDPIPPARL VALAGQGCVHCIECQTILEAQRR
1327619..1329859	PHAGE_Entero_phiFL4A: VirE domain protein	PP_01283	phage(gi281416460)	6.00E-51	MVDKHTLMDDVLAQLVDGGLEPETPLIPGKRVRCRAAGDKGKAK TGFYVIYEHVNEGRTFYAGAFGSWRE
1329856..1330230	hypothetical protein PFL_1990 [Pseudomonas protegens Pf-5] gi|70729371|ref|YP_259109.1|	PP_01284		1.00E-28	MIKYIDEALELWAAELHPPEGVEALGGGGGGSMLATLIACRGELIRS TRGSRVLLDESAEIELIVFKLLP
1330842..1331180	hypothetical protein PA14_07990 [Pseudomonas aeruginosa UCBPP-PA14] gi|116054342|ref|YP_788787.1|	PP_01285		1.00E-43	MPNEQQALAEMPVWVLILLAAAGGVSGEMWRADKAGLTGWVL LRRLALRSGASVVCGVAVMFLAMAMGAA
1331263..1331541	PHAGE_Cronob_ENT39118: HNH nuclease	PP_01286	phage(gi431811078)	2.00E-25	VFCLLEQRQTRAVLVDHKIAHRLGDAILSGDPERIAQARRLFWDRS NWQSLCKLCHDSTKQRMEKSGRVL
1331764..1332237	PHAGE_Tetras_SI1: terminase small subunit	PP_01287	phage(gi472342259)	5.00E-08	MLRGDPSKKGMAALQAAAQSPAVPVKAPPKPDHLSPEASAEWDR VVEALLALGWISELDGMALATYCEAV
1332200..1334026	PHAGE_Tetras_SI1: terminase	PP_01288	phage(gi472342258)	1.00E-98	MQNETQQTNTSADCRVAGFARAVLAGEIVAGPDVRNAARRHLQD LEDGHLRGLIWSQEAADRAIGFFEDV
1334023..1334202	PHAGE_Burkho_phi644_2: gp3, conserved hypothetical protein	PP_01289	phage(gi134288617)	3.00E-09	MKLLLLAWLAGLLGFGLLVAGVALISVPAAYIVAGLCLLAWSRLVDR AAAAQRAPGKGG
1334205..1335479	PHAGE_Burkho_phiE125: putative portal protein	PP_01290	phage(gi17975165)	6.00E-142	MFFSSILSGGQSTLVEDKGGLWRSLIGRGSNSSGVVVTPETALGLPIL QNCVTLLAESIAQLPLELYQRK
1335476..1336429	PHAGE_Burkho_phiE125: putative capsid assembly protein/protease	PP_01291	phage(gi17975166)	1.00E-95	MKRFLRASSLLFNQPLLVTPDMLDLGVRWANQAMNLNILNIGSAP APHMMEDDDYDHGARLERMQEQRRA
1336491..1337813	PHAGE_Burkho_phiE125: putative major capsid protein	PP_01292	phage(gi17975167)	3.00E-133	MSLVLQMRRERAELNDQLQALAKIEADGGSLTAEQMTQFGQLES QITALTDKISRAEIAERAAAASAVPV
1337871..1338212	PHAGE_Torque_teno_virus_27: hypothetical protein TTV27_gp3	PP_01293	phage(gi295413921)	2.00E-05	MSSNVSVRFLKAWRSYFKDDTAGFSQAVADELVAGGVAEYTDSAG STAAPAAKSQRRGKSGSKPAATGGA
1338215..1338766	PHAGE_Burkho_phiE125: hypothetical protein phiE125p08	PP_01294	phage(gi17975169)	8.00E-26	MARRIAYSGDAPITLADVARQCRVEVDDLEPELINLVIIPGVIAQAEG KTGAAVRPAEYVEDWPEHYPSG

1338948..1339319	hypothetical protein A458_06920 [Pseudomonas stutzeri CCUG 29243] gi|392420449|ref|YP_006457053.1|	PP_01295		2.00E-35	LRPGRYLCHGKRLLVITSVRDFRGDQAELILSCEELVGEPAEFRPADG PPVPCRVFITHSAPVFDDEQRV
1339334..1339930	hypothetical protein Pmen_3967 [Pseudomonas mendocina ymp] gi|146308981|ref|YP_001189446.1|	PP_01296		3.00E-30	MAGVELARAQLAEIGREVEPDLRLALNTTVRRGRKELYVPALLRFFP SRRFLNRSMVIKLAGTRRLNARI
1339989..1340423	hypothetical protein A458_06930 [Pseudomonas stutzeri CCUG 29243] gi|392420451|ref|YP_006457055.1|	PP_01297		6.00E-33	MPKATQLTVALKACLEGIKPSAGYVTEVRQVYGLLETPKDKAPTPYI KLRVADDRRTSTAGIQATRVRTY
1340452..1341240	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp010	PP_01298	phage(gi148912775)	4.00E-20	MSQTPYTQLFRGPTSICPYPSWNFEQIFRLQNIVGEPETSEVTVPDP TRPGLPELDGVTSFKAVNLTGEA
1341237..1341602	hypothetical protein A458_06945 [Pseudomonas stutzeri CCUG 29243] gi|392420454|ref|YP_006457058.1|	PP_01299		1.00E-19	MSDLSILFPKAEEVLLGRRRVEIRPVAFEHFAEFGAAAKGLIELVGAG STLEIATYAEQHAAELGKVVVH
1341599..1341778	hypothetical protein Pmen_3963 [Pseudomonas mendocina ymp] gi|146308977|ref|YP_001189442.1|	PP_01300		1.00E-06	LIGAGHCWADVRGYTLAQLEAFREAVDSEARESSRMALIITRAAQA KEKDYRKILKELS
1341778..1343973	PHAGE_Pseudo_F10: Putative tail length tape measure protein	PP_01301	phage(gi148912778)	7.00E-62	MAGRVTTQLIIEGKNTSNKAFAEVDKNLSKLNSKVSKVGEAIAAYLS FEALRSSVSAISEAADSVQLMNA
1344009..1344521	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp014	PP_01302	phage(gi148912779)	2.00E-37	MYRPTVMLGGVPLVIHAGPPTQRYSPLGGPEVIRLSQGAGVVMT HWARTAISLSGQGLMPLGLQGLDYRN
1359116..1359127	attR			N/A	tggccgtaagca
#### Prophage 4 ####					
complement(2736060..2737805)	PHAGE_Burkho_ST79: phage baseplate assembly protein V	PP_02649	phage(gi509141639)	2.00E-06	MPGLPEFDTRATNLTTFTVKADGTALSAEYEIVSVEIRREANRVPKA TVVLLDGDAAKQTFARSEEATLI
complement(2737810..2738517)	hypothetical protein HRM2_13150 [Desulfobacterium autotrophicum HRM2] gi|224368427|ref|YP_002602590.1|	PP_02650		4.00E-32	MDGALLKLTIIPFEDSEGAMGPPAGPPFIVQFNPETYTDTTEFKYGP DEPPQGSAGSEAKFERVNPKKYS
complement(2738521..2738703)	hypothetical	PP_02651		N/A	MPVFINEVVIRSTVDQPLPASGQQPTQTTGTPVDREALVAEVTQRV IDYLERELDRIGER
complement(2738714..2739154)	PHAGE_Bacill_BCD7: putative tail tube protein 2	PP_02652	phage(gi422936047)	2.00E-07	MSVYLPPVGFHFNARFDVPGATERDVRFRDVSGLTMELEEFAYNE GGENRFSHKLPVRGRYPDLVLKRGL
complement(2739162..2739593)	PHAGE_Bacill_BCD7: putative tail tube protein 2	PP_02653	phage(gi422936047)	6.00E-16	MSDYPLPKFHFQVQWGGARIGFTEISGLDVETEVIEYRDGALREFS KLKIPGMQKYPNVTMKRGVFKSDN
complement(2739612..2741078)	PHAGE_Bacill_BCD7: putative tail sheath protein	PP_02654	phage(gi422936048)	4.00E-28	MPSYSTPGVYVEEIPVFPPSVAPVATAIPAFIGYTEKAVGKQGEDLTK TAVRLTSLLEYEAWFGKPPVQD
complement(2741211..2741771)	hypothetical protein HRM2_13210 [Desulfobacterium autotrophicum HRM2] gi|224368433|ref|YP_002602596.1|	PP_02655		2.00E-19	MIADAVEFIRKEVRRHLGVANGDVIANSARKLAEEASAFGAYISMI NIEEEPVLRNTPHVEKRLGKSRYI
2742158..2742385	PHAGE_Entero_BP_4795: putative transposase OrfA protein of IS629	PP_02656	phage(gi157166066)	5.00E-15	MSKITTYSPEIREHAVRMILEHLNESPSEWAAIEAIAPRIDCAAQALR GWIRRHQTDAGQRPGATTEERE
complement(2743211..2743513)	PROPHAGE_Ralsto_GMI1000: ISRSO10-transposase ORFB protein	PP_02657	phage(gi17546154)	4.00E-40	VQWLSDNGSAYTAEQTRTFARQIGLLPLTTPVCSPQSNAMAESFVK TMKRDYIRHMPKPDRVTALRNLAI
complement(2743529..2743903)	PROPHAGE_Escher_CFT073: insertion element	PP_02658	phage(gi26249446)	2.00E-42	

	IS2 transposase InsD				LPSYGYRRVWGVLRRQHEQQAQPPVNVKRVYRVMRDHDLLLERRRKQPEVARRHKGRVAVDTSNTRWCSD
complement(2744010..2744570)	PHAGE_Thermo_THSA_485A: transcriptional regulator, XRE family	PP_02659	phage(gi397912660)	5.00E-05	LPNSTERPSVLVHVADNVKNLRRAADLSQDALAKASGVSRRMLVGIEAGDTNVSLATLDRIAAALDVTFA
2744663..2745550	hypothetical protein H681_11305 [Pseudomonas denitrificans ATCC 13867] gi|472325425|ref|YP_007657671.1|	PP_02660		7.00E-114	MPRSRFASLFYPVAVLMVSMASIQSGASLAKSLFPVLGAQGVTAMRLTFAAIILLVLLRPWRQPIARKSW
complement(2745552..2746451)	PHAGE_Burkho_phi1026b: gp58	PP_02661	phage(gi38707948)	7.00E-09	MKVQSDELRTFTTVIDSGSITAAADQLGLTASAVSRTLARLEEKLGTTLLNRTTRRMKLTEEGQFFLDSA
complement(2746902..2747666)	PHAGE_Tricho_ni_ascovirus_2c: hypothetical protein TNAV2c_gp071	PP_02662	phage(gi116326757)	7.00E-12	MDLGIAGRWAVVCAASKGLGKGCAKALAGEGVNLVINARGAEALEATAVELRQHNPNIEVRCVPGDVGQA
#### Prophage 5 ####					
5276653..5276666	attL			N/A	atcgccaaacgcca
complement(5282617..5282877)	PHAGE_Pseudo_PAJU2: hypothetical protein PAJU2_gp29	PP_05045	phage(gi209552448)	1.00E-30	MKWLVLWGLVALAGCAGQVEPEPRTVRVEVPVAVPCRAPAVEEPSWATAMLKKGDSLQVKVRALLAERQQ
complement(5282874..5283248)	PHAGE_Pseudo_PAJU2: hypothetical protein PAJU2_gp28	PP_05046	phage(gi209552447)	7.00E-25	MQSFPWKAAGLVLAVLLLVAAGAGLGVWLAAGHYRPQLDQSAQDLTTCRAARGNLETLVGDQNTAIAGLA
complement(5283258..5283671)	PHAGE_Pseudo_PAJU2: putative endolysin	PP_05047	phage(gi209552493)	7.00E-42	MGQDRDVDVLARTLWGEARGEGAAGMVAVGWTIRNRAAKPGWWGKDIVSVCQAPWQFSCWNKNDPNYLYL
complement(5283737..5284795)	PHAGE_Cyanop_S_TIM5: virion structural protein	PP_05048	phage(gi422936245)	2.00E-13	MADTFIPVRLSYTGSAVTAIAEYQPGETMQHPGNLNFSGSGRRITGDFSSPAGSVANRTWFQSNVTNGQT
complement(5285001..5285516)	PHAGE_Roseop_EE36P1: hypothetical protein EE36P1_gp32	PP_05049	phage(gi237651492)	6.00E-36	MAGDKYLTNNNGNLQEVVATQTSAGVANAGDIPALDASGRLDTSMMPVGLGADTAVITASEALAAGDYVN
complement(5285520..5286053)	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp022	PP_05050	phage(gi148912787)	4.00E-12	MSDAEQIEPWAVAVESDMPPLVLEQINEYAVTVTAGAELLVVTAGEQGPPGPQGNPGPAGGSALQKVAAV
complement(5286061..5286633)	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp021	PP_05051	phage(gi148912786)	2.00E-53	MQAARVPMCIARGATYRDTRRFMQPRREYRAISAIAPTAPLRLTAPGHGLDGDWLAWIAGASGFPNLNRE
complement(5286677..5287378)	hypothetical	PP_05052		N/A	MQYWLNNFSEPLVGALPSDEYSVLPLAQAALDALAALLPGKNDYVLLTLSSADGTGACEVIRYQPNGTIF
complement(5287388..5289220)	hypothetical protein Tgr7_0380 [Thioalkalivibrio sulfidophilus HL-EbGr7] gi|220933566|ref|YP_002512465.1|	PP_05053		3.00E-15	MNDEINILDLGQVRWWGHAIHGLALIGGTSPVYKASGLQFALPADIATSLVDAAVGIPNEDQGNVHLVKV
complement(5289220..5289546)	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp019	PP_05054	phage(gi148912784)	6.00E-05	MAGINQLKTDLNSLQAQDRQGRSLSPLEAKGSRPATKGRGDWQDPASTGTGGGIASPIVEVAARTYYAEQ
complement(5289549..5291282)	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp016	PP_05055	phage(gi148912781)	6.00E-128	MLINGAPLNSVPLNTLSSSSGTVEPVVPPLVVVWRCRLMLGGVDMTAQLTGTVRIEREEGAAAIAEFSIY
complement(5291283..5291792)	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp014	PP_05056	phage(gi148912779)	3.00E-38	MSLPMVMLGGVPIVPHAGSVSQSITPLGGPEIVRLSGGVGVPMTHWERSAIALSGSGWMPPGLDGLDYTQ
complement(5291837..5294431)	PHAGE_Pseudo_F10: Putative tail length tape measure protein	PP_05057	phage(gi148912778)	0	MTDIEVRLGADVDGATRNIGAFRTEYQKLVREIERPLGQIKAFRDLEDDLEGGARAAEEARSRVRDLGNE
complement(5294534..5294845)	PHAGE_Pseudo_F10: hypothetical protein	PP_05058		1.00E-18	

	PPF10_gp012		phage(gi148912777)		MSEVAGRKVVSIAGFEFTIKELTVAEVRALILGDGLDSEVDVAGDFL FEEIRLRDLLAFTTLTKAQVEQM
complement(5295241..5295993)	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp010	PP_05059	phage(gi148912775)	3.00E-99	MAQEKETFIIGGWLKARLAGTSDPFKKVGLVSTIQQAIETNDITLND TTTPQGGEYDAVSRITGMNLSIN
complement(5296032..5296496)	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp008	PP_05060	phage(gi148912773)	2.00E-40	MKPNLITEGRKAMIRRLGSITPANGYRTNAGERVSSGWLTDIVNQ DTSGFPLIVVQKARDLEPKPGPAAM
complement(5296493..5296807)	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp007	PP_05061	phage(gi148912772)	2.00E-18	MGWASMRDRLHRLAVTTFNDGVAQFTDKTGQRPPCGVPVVIDR NLAYEGADGIFVTGQVGFTWLKQDLAG
complement(5296811..5297164)	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp006	PP_05062	phage(gi148912771)	1.00E-06	MKTFIQNGDVITVPAPAGGTVSGKLYKVGAIVGVAATSEAAGDPVA LKTTGVFELTKTSAQAWAVGDLAY
complement(5297235..5299256)	PHAGE_Pseudo_F10: Putative Clp protease	PP_05063	phage(gi148912770)	1.00E-46	MTAKAQTFDTPLLQLRAAVRPDSVNIDDRTVEITWTTGAKGRRWS WDIGSYMEELEVSDSAVRLDRLNNG
complement(5299231..5300736)	PHAGE_Stenot_S1: putative portal protein	PP_05064	phage(gi213163905)	1.00E-72	MSILDTWLPGRAAKRAEARLRKKLAEQRLQLVERRFEGAAGGRRN EGWRSAGSDANAENAPALAVLRNRA
complement(5300738..5300941)	PHAGE_Stenot_S1: putative peptidase b	PP_05065	phage(gi213163904)	2.00E-07	MAYTLEQYEALKAAIAEGALSVRFADRQVTYRSIDEMIRILRLMESD LGLNANSNGGRRFASFSKGF
complement(5300941..5302887)	PHAGE_Pseudo_F10: Putative large subunit (GpA homolog) of DNA packaging dimer	PP_05066	phage(gi148912767)	0	MNISQPQLTEFAGSIRAGLKPLERPAPQTPVEWADDNFYLSSESSY QEGAWETLPFQVAILNAMGNDEIR
complement(5302859..5303392)	PHAGE_Pseudo_F10: Putative small subunit (Nu1 homolog) of DNA packaging dimer	PP_05067	phage(gi148912766)	1.00E-22	MATQIEVAKHLDLSDRQVRNLLADGVLPGSKGKGGFDIEACRLAYI RYLRGLGSSQVKPEADPDFPEGID
complement(5303549..5304301)	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp063	PP_05068	phage(gi148912828)	7.00E-94	VIVVGAAGLADQLAALDELEHDLIPYATSTALTKTAQGLIGRLQDEM RVVFDKPTPYTLNALRLMPATKD
complement(5304298..5304669)	PHAGE_Pseudo_PAJU2: hypothetical protein PAJU2_gp73	PP_05069	phage(gi209552492)	5.00E-28	MTEPASTAVGGIALYKLLSLLFGATFAAVVVMIMTRPKSTQEWAVA LISTVVSSVCGGAFLVRWLGIGSW
complement(5306507..5306872)	hypothetical protein PFLCHA0_c38160 [Pseudomonas protegens CHA0] gi|501681260|ref|YP_008001086.1|	PP_05070		2.00E-31	MQSFFRMTFGGLSAQYYFRQLFFGAIFLALLVWMQIMNPQKIRID VLVFSVICTLLYPYSRFVYERIVGF
complement(5306996..5307208)	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp058	PP_05071	phage(gi148912823)	4.00E-24	MKGKEGKRSTEVLMLSAEWYDINAWDTEARPDSTRSRWRRDIW KALDALEEQAVVRVTEILEREKLLSVA
complement(5307828..5309228)	PHAGE_Pseudo_F10: Putative DnaB-like replicative helicase	PP_05072	phage(gi148912819)	8.00E-93	MSRELYSLESEHGVLGAILRAAVQQDTALVDQVVETITAADFYFDD NAALFQTIADLHAEGVPVDPVTIA
complement(5309225..5310067)	PHAGE_Pseudo_F10: DNA replication protein DnaC	PP_05073	phage(gi148912818)	2.00E-43	MTARISNFVRAPERTQGPDNGAECPVHGRYTEVSVEQFDGGKLST GCPACHFAGLRTSPEGSEQHRQALQ
complement(5310048..5310344)	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp052	PP_05075	phage(gi148912817)	5.00E-31	LPDDWLAWALSERPEFGEAAMRKVGESFGDHWRAATGKGATKL DWQATWRNWVRNQRIPIGVQRAGPSLG
5310681..5310869	hypothetical	PP_05074		N/A	MRLLVLEEIRHLDDGKALDLVPTDEALIRERGKTFINVIVIPREEFHLD ALRAVLQPTFPIG
complement(5310968..5311081)	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp050	PP_05076	phage(gi148912815)	2.00E-07	VLYGSAKAYREALEGQGLAMSESYDDFIRRVTEELNI
complement(5311207..5311707)	hypothetical	PP_05077		N/A	MRLGAKLWEGTEMNNVAVHIDHVAPIISTSRTLFQVSIGQGLSRKA IYWFSFTDYELARQVFEMLSEDLL
5311971..5312105	hypothetical	PP_05078		N/A	MLNSSPLKFTLKVSSFNIRFQAWDQAEQRAIDLLAAGMDLAHLL
complement(5312247..5312567)	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp047	PP_05079	phage(gi148912812)	8.00E-40	VNARGFDVGANFQRALPGDGILFWFISTPAVQVNGLAVAQMVAP FPTEAEAQRGASLLNERYPGNNCWVG
complement(5312564..5312800)	PHAGE_Pseudo_F10: hypothetical protein	PP_05080		2.00E-28	

	PPF10_gp046		phage(gi148912811)		MDRVELTRHEFDLFNHARQDFNDLHVLLMEAVIPALGGGGHPVVSEIHDLFERVILHTGNFLFKYSQQIG
complement(5313324..5313941)	hypothetical protein PFLU2851 [Pseudomonas fluorescens SBW25] gi|229590311|ref|YP_002872430.1|	PP_05081		5.00E-40	MNTSNFRHSVTREGVLISFARDMIARTSISQDGFAESLNTTIFQLVPERAADRGYPDLVALTVTTDVPAY
5314676..5314861	hypothetical	PP_05082		N/A	VVEATSEEFDELLAQLNEAKKKASPKSQQTISRMIGMAERGELDDSAWKLINDLLTELAKK
5316706..5317221	PHAGE_Pseudo_F10: Conserved hypothetical protein	PP_05083	phage(gi148912824)	9.00E-44	MLELQLTNDDYRKMIQCEDGRLTTTSLKVAECFGKPHGKVLRDIRKLACSEGFRQANFGSSSYLNEQGKK
5317300..5317500	PHAGE_Pseudo_phi297: global regulatory protein	PP_05084	phage(gi374531265)	1.00E-14	MLILTRRVGETIRIGDDIEVTVLGYQGNQVRLGVTAPRDIEVHREEIYQRIHGAELRHQPKAVGSN
5317503..5318585	PHAGE_Pseudo_F10: Conserved hypothetical protein	PP_05085	phage(gi148912798)	1.00E-12	MNAVTIVLRSGMGMHLDAVRPYLNPGMPIAIGRAGAVIAEVADGNAIDDKRLAINSAAGYIDSAERYMES
5318582..5318806	hypothetical	PP_05086		N/A	VNSRAHWFWHCLLSVAAISFLGFFMAAIEQRDEARRLARPSIDMRGTTLVVSCPKPITPTAAPGAHPQQP
5318803..5319021	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp031	PP_05087	phage(gi148912796)	6.00E-06	MTLTAHVPAGAYSSPQPANPSPFYTLGARLVDLGTALQNERSTIDDLVRLASACGMDLRIKMVEDCSRAD
5319098..5319691	PHAGE_Pseudo_F10: hypothetical protein PPF10_gp030	PP_05088	phage(gi148912795)	5.00E-32	VARQFDQFDKVEGVVYSRASRSLKNGLPFTKGKLDKLEHDYRTLRKMRKAGRLAIGEWLMPAGAEIEAEL
5319688..5320404	PHAGE_Bacill_phBC6A51: hypothetical protein BC1875	PP_05089	phage(gi31415769)	4.00E-11	VKKRWLPADDERLRELYGTQSAEEVAELLGRTLSAVVSRASSLGLGKRPWTKADEDQLREIYPRSDMADI
5320642..5320655	attR			N/A	atcgccaaacgcca
5320902..5322020	PHAGE_Cronob_phiES15: putative integrase	PP_05090	phage(gi401817566)	1.00E-57	MYRGVRCRERIALKPTATNLKRAEQHKAAIEHAIANGTFDYSVTFPGSPRAAKFAPEASRETVAGFLGRW
5322087..5322530	PHAGE_Salmon_vB_SemP_Emek: hypothetical protein	PP_05091	phage(gi399498806)	2.00E-45	MPSSVDVAKFFLAQSNEEAGDLVSNLKLQKLVYYAQGFHLAVYDQPLFDDVIEAWTHGPVVPTVYHHYKA

Table S3. Predicted gene functions of ICE similar to ICE*clc* in five *Proteobacterial* genomes.

Location	Locus_tag	Product
ICE_NZ_KI5198281	***Pseudomonas aeruginosa* CF18**	**NZ_KI5198281.1**
1..1944	locus_tag="Q002_01712"	product="integrase"
complement(1982..2950)	locus_tag="Q002_01713"	product="Predicted dye-decolorizing peroxidase
complement(3069..3884)	locus_tag="Q002_01714"	product="hypothetical protein"
complement(4158..5048)	locus_tag="Q002_01715"	product="hypothetical protein"
complement(5518..6732)	locus_tag="Q002_01716"	product="formaldehyde dehydrogenase,
7050..7169	locus_tag="Q002_01717"	product="hypothetical protein"
complement(7199..8014)	locus_tag="Q002_01718"	product="hypothetical protein"
complement(9314..10585)	locus_tag="Q002_01719"	product="hypothetical protein"
11079..13055	locus_tag="Q002_01720"	product="excinuclease ABC subunit B"
complement(13206..14111)	locus_tag="Q002_01721"	product="Transcriptional regulator, LysR family"
14266..14673	locus_tag="Q002_01722"	product="hypothetical protein"
14675..15283	locus_tag="Q002_01723"	product="GNAT family acetyltransferase"
15280..16170	locus_tag="Q002_01724"	product="nitrilase"
16453..16728	locus_tag="Q002_01725"	product="regulator"
16788..17897	locus_tag="Q002_01726"	product="S-(hydroxymethyl)glutathione dehydrogenase"
17941..18339	locus_tag="Q002_01727"	product="glyoxalase"
18522..19856	locus_tag="Q002_01728"	product="hypothetical protein"
19915..20745	locus_tag="Q002_01729"	product="S-formylglutathione hydrolase"
20762..22069	locus_tag="Q002_01730"	product="NADH dehydrogenase"
22121..23434	locus_tag="Q002_01731"	product="hypothetical protein"
23489..25354	locus_tag="Q002_01732"	product="sodium:proton antiporter"
25431..28031	locus_tag="Q002_01733"	product="excinuclease ABC subunit A"
complement(28112..29956)	locus_tag="Q002_01734"	product="hypothetical protein"
30262..30579	locus_tag="Q002_01735"	product="AbrB family transcriptional regulator"
30579..31037	locus_tag="Q002_01736"	product="hypothetical protein"

31065..31442	locus_tag="Q002_01737"	product="hypothetical protein"
complement(31456..32973)	locus_tag="Q002_01738"	product="membrane protein"
complement(32989..33348)	locus_tag="Q002_01739"	product="hypothetical protein"
complement(33345..34742)	locus_tag="Q002_01740"	product="integrating conjugative element protein"
complement(34752..35699)	locus_tag="Q002_01741"	product="hypothetical protein"
complement(35696..36142)	locus_tag="Q002_01742"	product="hypothetical protein"
complement(36301..36795)	locus_tag="Q002_01743"	product="DNA repair protein RadC"
complement(36980..37744)	locus_tag="Q002_01744"	product="DSBA oxidoreductase"
complement(37758..40640)	locus_tag="Q002_01745"	product="conjugal transfer protein"
complement(40640..41080)	locus_tag="Q002_01746"	product="conjugal transfer protein"
complement(41061..42491)	locus_tag="Q002_01747"	product="signal peptide"
complement(42481..43398)	locus_tag="Q002_01748"	product="hypothetical protein"
complement(43395..44084)	locus_tag="Q002_01749"	product="hypothetical protein"
complement(44081..44491)	locus_tag="Q002_01750"	product="hypothetical protein"
complement(44504..44863)	locus_tag="Q002_01751"	product="hypothetical protein"
complement(44880..45113)	locus_tag="Q002_01752"	product="hypothetical protein"
complement(45110..45490)	locus_tag="Q002_01753"	product="hypothetical protein"
complement(45627..46529)	locus_tag="Q002_01754"	product="hypothetical protein"
46634..47308	locus_tag="Q002_01755"	product="hypothetical protein"
47460..48512	locus_tag="Q002_01756"	product="hypothetical protein"
48613..51237	locus_tag="Q002_01757"	product="ATPase"
complement(51267..52016)	locus_tag="Q002_01758"	product="membrane protein"
complement(52013..54199)	locus_tag="Q002_01759"	product="conjugal transfer protein TraG"
complement(54204..54752)	locus_tag="Q002_01760"	product="hypothetical protein"
complement(54749..55339)	locus_tag="Q002_01761"	product="lytic transglycosylase"
complement(55321..56046)	locus_tag="Q002_01762"	product="hypothetical protein"
complement(56061..56711)	locus_tag="Q002_01763"	product="hypothetical protein"
complement(56708..57169)	locus_tag="Q002_01764"	product="integrating conjugative element protein PilL,
57530..59314	locus_tag="Q002_01765"	product="ATP-dependent endonuclease"

59301..61115	locus_tag="Q002_01766"	product="ATP-dependent DNA helicase UvrD
complement(61182..61961)	locus_tag="Q002_01767"	product="hypothetical protein"
complement(62100..64379)	locus_tag="Q002_01768"	product="DEAD
complement(64517..64822)	locus_tag="Q002_01769"	product="hypothetical protein"
complement(64912..65232)	locus_tag="Q002_01770"	product="hypothetical protein"
complement(65283..66392)	locus_tag="Q002_01771"	product="O-methyl transferase"
complement(66457..67107)	locus_tag="Q002_01772"	product="hypothetical protein"
complement(67184..67444)	locus_tag="Q002_01773"	product="signal peptide protein"
complement(67461..67868)	locus_tag="Q002_01774"	product="hypothetical protein"
complement(67973..68314)	locus_tag="Q002_01775"	product="hypothetical protein"
complement(68409..69098)	locus_tag="Q002_01776"	product="hypothetical protein"
complement(69194..70021)	locus_tag="Q002_01777"	product="hypothetical protein"
complement(70174..71103)	locus_tag="Q002_01778"	product="hypothetical protein"
complement(71449..71727)	locus_tag="Q002_01779"	product="uridylate kinase"
complement(71824..72561)	locus_tag="Q002_01780"	product="ABC transporter substrate-binding protein"
complement(72776..73168)	locus_tag="Q002_01781"	product="hypothetical protein"
complement(73190..73402)	locus_tag="Q002_01782"	product="hypothetical protein"
complement(74325..76346)	locus_tag="Q002_01783"	product="DNA topoisomerase III"
complement(76626..77066)	locus_tag="Q002_01784"	product="single-stranded DNA-binding protein"
complement(77140..77667)	locus_tag="Q002_01785"	product="integrase"
complement(77664..78443)	locus_tag="Q002_01786"	product="hypothetical protein"
complement(78775..80025)	locus_tag="Q002_01787"	product="hypothetical protein"
complement(80029..80589)	locus_tag="Q002_01788"	product="hypothetical protein"
complement(80605..82269)	locus_tag="Q002_01789"	product="hypothetical protein"
complement(82262..82522)	locus_tag="Q002_01790"	product="hypothetical protein"
complement(82506..83381)	locus_tag="Q002_01791"	product="cobyrinic acid a,c-diamide synthase"
complement(83424..83636)	locus_tag="Q002_01792"	product="transcriptional regulator"
complement(83755..84501)	locus_tag="Q002_01793"	product="hypothetical protein"
85227..85550	locus_tag="Q002_01794"	product="ArsR family transcriptional regulator"

85555..86049	locus_tag="Q002_01795"	product="ArsR family transcriptional regulator"
86060..87130	locus_tag="Q002_01796"	product="arsenic transporter"
87133..88365	locus_tag="Q002_01797"	product="MFS transporter"
88362..88784	locus_tag="Q002_01798"	product="arsenate reductase"
88762..89499	locus_tag="Q002_01799"	product="NADPH-dependent FMN reductase"
90506..91425	locus_tag="Q002_01800"	product="two-component system sensor
ICE_NC_014640	***Achromobacter xylosoxidans* A8**	**NC_014640.1**
83343..83957	locus_tag="AXYL_01047"	product="hypothetical protein"
complement(84131..84131)	locus_tag="AXYL_01046"	product="outer membrane autotransporter barrel
complement(81637..82383)	locus_tag="AXYL_01048"	product="receptor protein-tyrosine kinase"
complement(81306..81518)	locus_tag="AXYL_01049"	product="prophage CP4-57 regulatory protein AlpA"
complement(80388..81263)	locus_tag="AXYL_01050"	product="CobQ
complement(80144..80404)	locus_tag="AXYL_01051"	product="hypothetical protein"
complement(78487..80151)	locus_tag="AXYL_01052"	product="hypothetical protein"
complement(77911..78471)	locus_tag="AXYL_01053"	product="hypothetical protein"
complement(76657..77907)	locus_tag="AXYL_01054"	product="hypothetical protein"
complement(75537..76325)	locus_tag="AXYL_01055"	product="hypothetical protein"
complement(75013..75540)	locus_tag="AXYL_01056"	product="hypothetical protein"
complement(74487..74939)	locus_tag="AXYL_01057"	product="single-strand binding family protein"
complement(72180..74210)	locus_tag="AXYL_01058"	product="DNA topoisomerase III 1"
complement(70038..71648)	locus_tag="AXYL_01059"	product="methyltransferase"
complement(69237..69995)	locus_tag="AXYL_01060"	product="hypothetical protein"
complement(68682..68903)	locus_tag="AXYL_01061"	product="hypothetical protein"
complement(68268..68660)	locus_tag="AXYL_01062"	product="hypothetical protein"
complement(67399..68085)	locus_tag="AXYL_01063"	product="hypothetical protein"
complement(66578..67315)	locus_tag="AXYL_01064"	product="hypothetical protein"
complement(66202..66480)	locus_tag="AXYL_01065"	product="hypothetical protein"
complement(65089..65913)	locus_tag="AXYL_01066"	product="hypothetical protein"

64420..64827	locus_tag="AXYL_01067"	product="Hg(II)-responsive transcriptional regulator"
complement(63998..64348)	locus_tag="AXYL_01068"	product="mercuric transporter"
complement(63698..63985)	locus_tag="AXYL_01069"	product="mercuric transporter periplasmic component"
complement(61999..63687)	locus_tag="AXYL_01070"	product="mercuric reductase"
complement(60653..60913)	locus_tag="AXYL_01073"	product="hypothetical protein"
complement(60061..60345)	locus_tag="AXYL_01074"	product="hypothetical protein"
complement(58845..59750)	locus_tag="AXYL_01075"	product="hypothetical protein"
complement(57872..58699)	locus_tag="AXYL_01076"	product="hypothetical protein"
complement(57088..57777)	locus_tag="AXYL_01077"	product="hypothetical protein"
complement(56652..56993)	locus_tag="AXYL_01078"	product="hypothetical protein"
complement(56140..56547)	locus_tag="AXYL_01079"	product="hypothetical protein"
complement(55863..56123)	locus_tag="AXYL_01080"	product="hypothetical protein"
complement(55139..55786)	locus_tag="AXYL_01081"	product="hypothetical protein"
complement(53965..55074)	locus_tag="AXYL_01082"	product="O-methyl transferase family protein"
complement(53594..53914)	locus_tag="AXYL_01083"	product="O-methyl transferase family domain-containing
complement(53199..53504)	locus_tag="AXYL_01084"	product="hypothetical protein"
complement(50783..53062)	locus_tag="AXYL_01085"	product="helicase"
50001..50723	locus_tag="AXYL_01086"	product="arsenic resistance protein ArsH"
49586..50008	locus_tag="AXYL_01087"	product="arsenate reductase 1"
48493..49569	locus_tag="AXYL_01088"	product="sodium bile acid symporter family protein 1"
47988..48482	locus_tag="AXYL_01089"	product="low molecular weight phosphotyrosine protein
47647..47985	locus_tag="AXYL_01090"	product="ArsR family transcriptional regulator"
complement(46930..47496)	locus_tag="AXYL_01091"	product="PilL protein"
complement(46289..46933)	locus_tag="AXYL_01092"	product="hypothetical protein"
complement(45549..46274)	locus_tag="AXYL_01093"	product="hypothetical protein"
complement(44977..45567)	locus_tag="AXYL_01094"	product="transglycosylase SLT domain-containing protein
complement(44441..44980)	locus_tag="AXYL_01095"	product="hypothetical protein"
complement(42247..44436)	locus_tag="AXYL_01096"	product="hypothetical protein"
complement(41501..42250)	locus_tag="AXYL_01097"	product="hypothetical protein"

complement(41019..41402)	locus_tag="AXYL_01098"	product="hypothetical protein"
complement(40789..41022)	locus_tag="AXYL_01099"	product="hypothetical protein"
complement(40413..40772)	locus_tag="AXYL_01100"	product="hypothetical protein"
complement(40003..40401)	locus_tag="AXYL_01101"	product="hypothetical protein"
complement(39314..40006)	locus_tag="AXYL_01102"	product="hypothetical protein"
complement(38406..39317)	locus_tag="AXYL_01103"	product="hypothetical protein"
complement(36998..38416)	locus_tag="AXYL_01104"	product="hypothetical protein"
complement(36568..37017)	locus_tag="AXYL_01105"	product="signal recognition particle GTPase"
complement(33674..36568)	locus_tag="AXYL_01106"	product="type IV secretory pathway, VirB4 component"
complement(32896..33660)	locus_tag="AXYL_01107"	product="hypothetical protein"
complement(32226..32720)	locus_tag="AXYL_01108"	product="DNA repair protein RadC 1"
complement(31616..32008)	locus_tag="AXYL_01109"	product="hypothetical protein"
complement(30669..31619)	locus_tag="AXYL_01110"	product="hypothetical protein"
complement(29265..30659)	locus_tag="AXYL_01111"	product="hypothetical protein"QVQRT
complement(28897..29268)	locus_tag="AXYL_01112"	product="hypothetical protein"
complement(27366..28883)	locus_tag="AXYL_01113"	product="TraG-like family protein"
26973..27350	locus_tag="AXYL_01114"	product="hypothetical protein"
26488..26946	locus_tag="AXYL_01115"	product="hypothetical protein"
26171..26488	locus_tag="AXYL_01116"	product="AbrB family transcriptional regulator"
complement(23994..25871)	locus_tag="AXYL_01117"	product="hypothetical protein"
complement(23773..23910)	locus_tag="AXYL_01118"	product="hypothetical protein"
complement(23482..23739)	locus_tag="AXYL_01119"	product="copper-translocating P-type ATPase 1"
22086..23522	locus_tag="AXYL_01120"	product="sensor kinase CusS"
21422..22114	locus_tag="AXYL_01121"	product="transcriptional activator protein IrlR 2"
21306..21425	locus_tag="AXYL_01122"	product="hypothetical protein"
complement(19264..21168)	locus_tag="AXYL_01123"	product="copper resistance protein A"
complement(18258..19238)	locus_tag="AXYL_01124"	product="copper resistance protein B domain-containing
complement(17735..18220)	locus_tag="AXYL_01125"	product="hypothetical protein"
complement(17429..17701)	locus_tag="AXYL_01126"	product="hypothetical protein"

complement(14835..17141)	locus_tag="AXYL_01127"	product="copper-translocating P-type ATPase 2"
complement(14307..14693)	locus_tag="AXYL_01128"	product="copper resistance protein C"
complement(13376..14302)	locus_tag="AXYL_01129"	product="copper resistance protein D"
complement(12963..13247)	locus_tag="AXYL_01130"	product="hypothetical protein"
complement(11841..12731)	locus_tag="AXYL_01131"	product="transcriptional regulator 2"
11531..11836	locus_tag="AXYL_01132"	product="hypothetical protein"
complement(10782..11423)	locus_tag="AXYL_01133"	product="LysR family transcriptional regulator"
10704..10946	locus_tag="AXYL_01134"	product="hypothetical protein"
complement(10184..10495)	locus_tag="AXYL_01135"	product="hypothetical protein"
complement(9054..10031)	locus_tag="AXYL_01136"	product="transposase, IS4 family protein 1"
complement(7646..8881)	locus_tag="AXYL_01137"	product="heavy metal RND efflux outer membrane protein,
complement(6119..7630)	locus_tag="AXYL_01138"	product="RND family efflux transporter MFP subunit 3"
complement(3006..6122)	locus_tag="AXYL_01139"	product="cation efflux system protein CusA"
2615..2845	locus_tag="AXYL_01140"	product="LysR family transcriptional regulator"
314..2257	locus_tag="AXYL_01141"	product="integrase"
ICE_NZ_HE_983628	***Bordetella bronchiseptica* Bbr77**	**NZ_HE_983628.1**
complement(94779..95525)	locus_tag="BN116_4126"	product="putative uncharacterized protein"
complement(94448..94660)	locus_tag="BN116_4127"	product="phage-related protein"
complement(93530..94405)	locus_tag="BN116_4128"	product="chromosome partitioning related protein"
complement(93298..93546)	locus_tag="BN116_4129"	product="putative uncharacterized protein"
complement(91668..93296)	locus_tag="BN116_4130"	product="putative uncharacterized protein"
complement(91092..91652)	locus_tag="BN116_4131"	product="putative uncharacterized protein"
complement(89827..91089)	locus_tag="BN116_4132"	product="putative uncharacterized protein"
complement(88738..89511)	locus_tag="BN116_4133"	product="putative transposon"
complement(88214..88741)	locus_tag="BN116_4134"	product="putative uncharacterized protein"
complement(87688..88140)	locus_tag="BN116_4135"	product="single-stranded DNA-binding protein"
complement(85389..87413)	locus_tag="BN116_4136"	product="dna topoisomerase ec=5.99.1.2"
complement(83253..84851)	locus_tag="BN116_4137"	product="dna-cytosine methyltransferase ec=2.1.1.37"

complement(82452..83204)	locus_tag="BN116_4138"	product="putative uncharacterized protein"
complement(81897..82295)	locus_tag="BN116_4139"	product="putative uncharacterized protein"
complement(81482..81874)	locus_tag="BN116_4140"	product="putative uncharacterized protein"
complement(80652..81338)	locus_tag="BN116_4141"	product="putative uncharacterized protein"
complement(79834..80571)	locus_tag="BN116_4142"	product="putative uncharacterized protein"
complement(79461..79739)	locus_tag="BN116_4143"	product="putative uncharacterized protein"
complement(78373..79176)	locus_tag="BN116_4144"	product="putative uncharacterized protein"
complement(77941..78294)	locus_tag="BN116_4145"	product="putative uncharacterized protein"
complement(76662..77804)	locus_tag="BN116_4146"	product="putative uncharacterized protein"
complement(75915..76604)	locus_tag="BN116_4147"	product="putative uncharacterized protein"
complement(75497..75820)	locus_tag="BN116_4148"	product="conserved plasmid protein"
complement(74989..75396)	locus_tag="BN116_4149"	product="conserved hypothetical protein"
complement(74712..74972)	locus_tag="BN116_4150"	product="putative uncharacterized protein"
complement(73985..74635)	locus_tag="BN116_4151"	product="putative uncharacterized protein"
complement(72811..73920)	locus_tag="BN116_4152"	product="putative uncharacterized protein"
complement(72396..72707)	locus_tag="BN116_4153"	product="putative uncharacterized protein"
complement(70014..72320)	locus_tag="BN116_4154"	product="conserved plasmid related protein"
complement(69031..69900)	locus_tag="BN116_4155"	product="putative uncharacterized protein"QVVVVDMTDGQIHSIR
complement(68273..68872)	locus_tag="BN116_4156"	product="hypothetical protein"
complement(67635..68276)	locus_tag="BN116_4157"	product="hypothetical protein"
complement(66895..67620)	locus_tag="BN116_4158"	product="conserved protein, putatively exported"
complement(66323..66913)	locus_tag="BN116_4159"	product="lytic transglycosylase"
complement(65787..66326)	locus_tag="BN116_4160"	product="putative exported protein"
complement(63590..65782)	locus_tag="BN116_4161"	product="putative plasmid-transfer-protein"
complement(62832..63593)	locus_tag="BN116_4162"	product="membrane protein"
61856..62785	locus_tag="BN116_4163"	product="putative uncharacterized protein"
complement(61267..61647)	locus_tag="BN116_4164"	product="putative membrane protein"
complement(61037..61270)	locus_tag="BN116_4165"	product="putative uncharacterized protein"
complement(60661..61020)	locus_tag="BN116_4166"	product="putative uncharacterized protein"

complement(60238..60648)	locus_tag="BN116_4167"	product="putative uncharacterized protein"
complement(59549..60241)	locus_tag="BN116_4168"	product="putative uncharacterized protein"
complement(58635..59552)	locus_tag="BN116_4169"	product="putative secreted protein"
complement(57227..58645)	locus_tag="BN116_4170"	product="putative exported protein"
complement(56806..57246)	locus_tag="BN116_4171"	product="conjugal transfer protein"
complement(53930..56806)	locus_tag="BN116_4172"	product="putative uncharacterized protein"
complement(53131..53916)	locus_tag="BN116_4173"	product="putative uncharacterized protein"
complement(52454..52948)	locus_tag="BN116_4174"	product="DNA repair protein RadC"
complement(51845..52291)	locus_tag="BN116_4175"	product="putative secreted protein"
complement(50901..51848)	locus_tag="BN116_4176"	product="putative uncharacterized protein"
complement(49494..50891)	locus_tag="BN116_4177"	product="putative uncharacterized protein"
complement(49126..49497)	locus_tag="BN116_4178"	product="hypothetical protein"
complement(47590..49110)	locus_tag="BN116_4179"	product="membrane protein"
47213..47578	locus_tag="BN116_4180"	product="hypothetical protein"
46496..47128	locus_tag="BN116_4181"	product="putative uncharacterized protein"
45857..46483	locus_tag="BN116_4182"	product="integrase"
complement(43669..45540)	locus_tag="BN116_4183"	product="relaxase"
42746..43618	locus_tag="BN116_4184"	product="2-dehydro-3-deoxyphosphooctonate aldolase"
42314..42571	locus_tag="BN116_4185"	product="glutaredoxin"
41602..42303	locus_tag="BN116_4186"	product="hypothetical protein"
40160..40855	locus_tag="BN116_4187"	product="GntR family transcriptional regulator"
complement(39418..39960)	locus_tag="BN116_4188"	product="putative uncharacterized protein flags:
complement(38733..39236)	locus_tag="BN116_4189"	product="hypothetical protein"
36009..37463	locus_tag="BN116_4190"	product="mercuric reductase"
35602..35742	locus_tag="BN116_4191"	product="putative uncharacterized protein"
join(34131..34271,34506..35138)	locus_tag="BN116_4192"	product="major facilitator superfamily MFS_1,
31506..33011	locus_tag="BN116_4193"	product="multidrug transporter"
join(28304..29188,28939..3148	locus_tag="BN116_4194"	product="hydrophobe

5)		
27000..28307	locus_tag="BN116_4195"	product="transporter"
24180..26888	locus_tag="BN116_4196"	product="heavy metal translocating P-type ATPase"
23444..24013	locus_tag="BN116_4197"	product="putative uncharacterized protein"
22837..23214	locus_tag="BN116_4198"	product="ArsR family transcriptional regulator"
21771..22793	locus_tag="BN116_4199"	product="zinc transporter ZitB"
20327..21637	locus_tag="BN116_4200"	product="major facilitator transporter"
20060..20317	locus_tag="BN116_4201"	product="putative uncharacterized protein"
complement(18449..19777)	locus_tag="BN116_4202"	product="outer membrane efflux protein flags: precursor"
complement(16751..17866)	locus_tag="BN116_4203"	product="membrane protein"
complement(13591..16737)	locus_tag="BN116_4204"	product="heavy metal efflux pump, czca family flags:
complement(11606..13033)	locus_tag="BN116_4205"	product="dihydrolipoamide dehydrogenase"
11140..11496	locus_tag="BN116_4206"	product="putative uncharacterized protein"
complement(8409..10934)	locus_tag="BN116_4207"	product="copper-transporting p-type atpase ec=3.6.3.4"
complement(7914..8393)	locus_tag="BN116_4208"	product="transcriptional regulator, merr family"
complement(7560..7898)	locus_tag="BN116_4209"	product="[2fe-2s] ferredoxin"
complement(6578..7303)	locus_tag="BN116_4210"	product="putative uncharacterized protein"
6309..6503	locus_tag="BN116_4211"	product="putative uncharacterized protein"
5699..6208	locus_tag="BN116_4212"	product="transcriptional regulator, asnc family"
complement(4506..5594)	locus_tag="BN116_4213"	product="4-hydroxyphenylpyruvate dioxygenase"
complement(3292..4185)	locus_tag="BN116_4214"	product="transcriptional regulator, lysr family"
2972..3265	locus_tag="BN116_4215"	product="predicted transcriptional regulator"
186..2171	locus_tag="BN116_4216"	product="phage-related integrase"
ICE_NC_007508	***Xanthomonas campestris***	**NC_007508.1**
locus_tag="XCV_tRNA36"	locus_tag="XCV_tRNA36"	product="tRNA-Gly"
303..2246	locus_tag="XCV2298"	product="phage-related integrase"
complement(2296..2937)	locus_tag="XCV2299"	product="LysR family transcriptional regulator"
3042..3335	locus_tag="XCV2300"	product="hypothetical protein"

complement(3342..4232)	locus_tag="XCV2301"	product="LysR family transcriptional regulator"
complement(4269..4592)	locus_tag="XCV2302"	product="hypothetical protein"
complement(4630..5997)	locus_tag="XCV2303"	product="dihydrolipoamide dehydrogenase"
complement(6038..6844)	locus_tag="XCV2304"	product="hypothetical protein"
complement(6863..7375)	locus_tag="XCV2305"	product="hypothetical protein"
complement(7471..8244)	locus_tag="XCV2306"	product="disulfide isomerase
complement(8247..9083)	locus_tag="XCV2307"	product="thiol disulfide interchange protein"
complement(9083..10873)	locus_tag="XCV2308"	product="thiol:disulfide interchange protein"
11068..11736	locus_tag="XCV2309"	product="two-component system regulatory protein"
11733..13091	locus_tag="XCV2310"	product="two-component system sensor protein"
complement(13155..14114)	locus_tag="XCV2311"	product="thioredoxin reductase"
complement(14156..14608)	locus_tag="XCV2312"	product="hypothetical protein"
complement(14758..15078)	locus_tag="XCV2313"	product="thioredoxin"
15269..15952	locus_tag="XCV2314"	product="ArsR family transcriptional regulator"
complement(15970..16614)	locus_tag="XCV2315"	product="thiol:disulfide interchange protein"
complement(16678..17577)	locus_tag="XCV2316"	product="hypothetical protein"
complement(17716..18180)	locus_tag="XCV2317"	product="hypothetical protein"
complement(18290..19267)	locus_tag="XCV2318"	product="potassium-tellurite ethidium and proflavin
complement(19355..19612)	locus_tag="XCV2319"	product="hypothetical protein"
19840..20634	locus_tag="XCV2320"	product="IS6100 transposase"
complement(20606..21004)	locus_tag="XCV2321"	product="transposase (fragment)"
21210..22937	locus_tag="XCV2322"	product="transposase"
23033..23917	locus_tag="XCV2323"	product="LysR family transcriptional regulator"
complement(24216..24773)	locus_tag="XCV2324"	product="hypothetical protein"
complement(24935..25780)	locus_tag="XCV2325"	product="streptomycin 3''-kinase"
complement(25771..26574)	locus_tag="XCV2326"	product="streptomycin 3''-kinase"
complement(26640..27254)	locus_tag="XCV2327"	product="resolvase"
complement(27358..27756)	locus_tag="XCV2328"	product="TniQ-related transposition protein"
complement(27798..28592)	locus_tag="XCV2329"	product="IS6100 transposase"

28591..29085	locus_tag="XCV2330"	product="hypothetical protein"ADPDGGTELLVLSGEMMVDDQR
29088..30236	locus_tag="XCV2331"	product="amine oxidase"
30255..31433	locus_tag="XCV2332"	product="aminotransferase"
31470..32498	locus_tag="XCV2333"	product="Zn-dependent alcohol dehydrogenase"
32551..33780	locus_tag="XCV2334"	product="major facilitator superfamily protein"
complement(33854..34333)	locus_tag="XCV2335"	product="MerR family transcriptional regulator"
complement(34349..36850)	locus_tag="XCV2336"	product="copper-translocating P-type ATPase"
37018..37371	locus_tag="XCV2337"	product="ArsR family transcriptional regulator"
37560..38561	locus_tag="XCV2338"	product="cobalt-zinc-cadmium resistance protein"
38883..39974	locus_tag="XCV2339"	product="major facilitator superfamily protein"
complement(39993..40787)	locus_tag="XCV2340"	product="IS6100 transposase"
complement(40723..41607)	locus_tag="XCV2341"	product="hypothetical protein"
complement(41604..42512)	locus_tag="XCV2342"	product="transposition protein TniB"
complement(42515..44233)	locus_tag="XCV2343"	product="transposase"
44418..44639	locus_tag="XCV2344"	product="hypothetical protein"
44632..45633	locus_tag="XCV2345"	product="cytosine-specific DNA methylase"
complement(45882..46724)	locus_tag="XCV2346"	product="AraC family transcriptional regulator"
46800..47375	locus_tag="XCV2347"	product="hypothetical protein"
47567..47806	locus_tag="XCV2348"	product="hypothetical protein"
complement(47803..48096)	locus_tag="XCV2349"	product="transposase (fragment)"
complement(48297..49313)	locus_tag="XCV2350"	product="major facilitator superfamily protein"
49398..50429	locus_tag="XCV2351"	product="transposase"
complement(50561..51001)	locus_tag="XCV2352"	product="carboxymuconolactone decarboxylase"
51104..51898	locus_tag="XCV2353"	product="IS6100 transposase"
52046..52981	locus_tag="XCV2354"	product="LysR family transcriptional regulator"
53238..53735	locus_tag="XCV2355"	product="hypothetical protein"
complement(53800..55632)	locus_tag="XCV2356"	product="hypothetical protein"
55946..56572	locus_tag="XCV2357"	product="hypothetical protein"
56585..57202	locus_tag="XCV2358"	product="hypothetical protein"

57302..57664	locus_tag="XCV2359"	product="hypothetical protein"
complement(57671..59194)	locus_tag="XCV2360"	product="hypothetical protein"
complement(59209..59580)	locus_tag="XCV2361"	product="hypothetical protein"
complement(59577..60974)	locus_tag="XCV2362"	product="hypothetical protein"
complement(60984..61931)	locus_tag="XCV2363"	product="hypothetical protein"
complement(61928..62374)	locus_tag="XCV2364"	product="hypothetical protein"
complement(62537..63031)	locus_tag="XCV2365"	product="RadC family DNA repair protein"
complement(63213..63998)	locus_tag="XCV2366"	product="hypothetical protein"
complement(64012..66879)	locus_tag="XCV2367"	product="hypothetical protein"
complement(66879..67319)	locus_tag="XCV2368"	product="hypothetical protein"
complement(68720..69634)	locus_tag="XCV2370"	product="hypothetical protein"
complement(69631..70323)	locus_tag="XCV2371"	product="hypothetical protein"
complement(70320..70718)	locus_tag="XCV2372"	product="hypothetical protein"
complement(70731..71087)	locus_tag="XCV2373"	product="hypothetical protein"
complement(71105..71338)	locus_tag="XCV2374"	product="hypothetical protein"
complement(71335..71715)	locus_tag="XCV2375"	product="hypothetical protein"
complement(71814..72563)	locus_tag="XCV2376"	product="hypothetical protein"
complement(72560..74752)	locus_tag="XCV2377"	product="hypothetical protein"
complement(74757..75296)	locus_tag="XCV2378"	product="hypothetical protein"
complement(75293..75883)	locus_tag="XCV2379"	product="lytic transglycosylase precursor"
complement(75865..76590)	locus_tag="XCV2380"	product="hypothetical protein"
complement(76603..77172)	locus_tag="XCV2381"	product="hypothetical protein"
complement(77226..77825)	locus_tag="XCV2382"	product="hypothetical protein"
complement(78014..79102)	locus_tag="XCV2383"	product="hypothetical protein"
complement(79119..81314)	locus_tag="XCV2384"	product="cytochrome precursor"
complement(81642..82328)	locus_tag="XCV2385"	product="hypothetical protein"VVDMTDGQIHSIR
complement(82440..84719)	locus_tag="XCV2386"	product="helicase"
complement(84855..85160)	locus_tag="XCV2387"	product="hypothetical protein"
complement(85251..85571)	locus_tag="XCV2388"	product="hypothetical protein"

complement(85623..86732)	locus_tag="XCV2389"	product="hypothetical protein"
complement(86797..87447)	locus_tag="XCV2390"	product="hypothetical protein"
complement(87524..87784)	locus_tag="XCV2391"	product="hypothetical protein"
complement(87801..88208)	locus_tag="XCV2392"	product="hypothetical protein"
complement(88309..88632)	locus_tag="XCV2393"	product="hypothetical protein"
complement(88727..89416)	locus_tag="XCV2394"	product="hypothetical protein"
complement(89474..90706)	locus_tag="XCV2395"	product="hypothetical protein"
complement(90757..91110)	locus_tag="XCV2396"	product="hypothetical protein"
complement(91190..91411)	locus_tag="XCV2397"	product="hypothetical protein"
complement(91408..92220)	locus_tag="XCV2398"	product="hypothetical protein"
complement(92503..92781)	locus_tag="XCV2399"	product="hypothetical protein"
complement(92879..93616)	locus_tag="XCV2400"	product="hypothetical protein"
complement(93696..94382)	locus_tag="XCV2401"	product="hypothetical protein"
complement(94528..94920)	locus_tag="XCV2402"	product="hypothetical protein"
complement(94942..95328)	locus_tag="XCV2403"	product="hypothetical protein"
complement(95486..96238)	locus_tag="XCV2404"	product="hypothetical protein"
complement(96287..97903)	locus_tag="XCV2405"	product="DNA methyltransferase"
complement(98437..100449)	locus_tag="XCV2406"	product="DNA topoisomerase III"
complement(100723..101175)	locus_tag="XCV2407"	product="single-stranded DNA-binding protein"
complement(101249..101776)	locus_tag="XCV2408"	product="hypothetical protein"
complement(101773..102555)	locus_tag="XCV2409"	product="hypothetical protein"
complement(102872..104119)	locus_tag="XCV2410"	product="hypothetical protein"
complement(104122..104682)	locus_tag="XCV2411"	product="hypothetical protein"
complement(104698..106353)	locus_tag="XCV2412"	product="hypothetical protein"
complement(106346..106594)	locus_tag="XCV2413"	product="hypothetical protein"
complement(106578..107453)	locus_tag="XCV2414"	product="chromosome partitioning-like protein"
complement(107496..107708)	locus_tag="XCV2415"	product="AlpA family regulatory protein"
complement(107827..108582)	locus_tag="XCV2416"	product="hypothetical protein"
109890..111182	locus_tag="XCV2417"	product="UDP-glucose

complement(111166..112428)	locus_tag="XCV2418"	product="hypothetical protein"
complement(112439..112882)	locus_tag="XCV2419"	product="FKBP-type peptidyl-prolyl cis-trans isomerase"
112930..113295	locus_tag="XCV2420"	product="hypothetical protein"
113395..114141	locus_tag="XCV2421"	product="rhodanese superfamily protein"
114381..115028	locus_tag="XCV2422"	product="LuxR family two-component response regulator"
complement(115553..119203)	locus_tag="XCV2423"	product="ribonuclease E"
119604..120590	locus_tag="XCV2424"	product="pseudouridylate synthase"
complement(120624..122441)	locus_tag="XCV2425"	product="hypothetical protein"
complement(122739..123557)	locus_tag="XCV2426"	product="zinc transporter ZupT"
complement(123822..124244)	locus_tag="XCV2427"	product="hypothetical protein"
complement(124241..124597)	locus_tag="XCV2428"	product="pterin-4-alpha-carbinolamine dehydratase"
124686..125285	locus_tag="XCV2429"	product="thioredoxin-like protein"
125299..127125	locus_tag="XCV2430"	product="hypothetical protein"
complement(127420..127989)	locus_tag="XCV2431"	product="TetR family transcriptional regulator"
128113..128354	locus_tag="XCV2432"	product="membrane fusion protein"
ICE_NC_008344	***Nitrosomonas eutropha* C91**	**NC_008344.1**
	locus_tag="Neut_R0001"	product="tRNA-Gly"
302..2155	locus_tag="Neut_0006"	product="phage integrase family protein"
2242..2616	locus_tag="Neut_0007"	product="LysR family transcriptional regulator"
complement(3110..3769)	locus_tag="Neut_0008"	product="LysR family transcriptional regulator"
4138..4440	locus_tag="Neut_0009"	product="XRE family transcriptional regulator protein"
complement(5007..5840)	locus_tag="Neut_0010"	product="redoxin domain-containing protein"
complement(6128..7036)	locus_tag="Neut_0011"	product="LysR family transcriptional regulator"
7174..7497	locus_tag="Neut_0012"	product="transposase IS3
7551..8402	locus_tag="Neut_0013"	product="integrase catalytic subunit"
complement(9064..10686)	locus_tag="Neut_0014"	product="twin-arginine translocation pathway signal"
11313..11783	locus_tag="Neut_0016"	product="transposase, IS4 family protein"
complement(12003..13415)	locus_tag="Neut_0017"	product="heavy metal sensor signal transduction

complement(13421..14104)	locus_tag="Neut_0018"	product="two component heavy metal response
complement(14490..14690)	locus_tag="Neut_0019"	product="heavy metal transport
15354..16325	locus_tag="Neut_0020"	product="BNR repeat-containing glycosyl hydrolase"
16676..18559	locus_tag="Neut_0021"	product="copper-resistance protein, CopA family protein"
19750..20298	locus_tag="Neut_0023"	product="blue (type1) copper domain-containing protein"
20500..21081	locus_tag="Neut_0024"	product="peptidase M23B"
21163..21648	locus_tag="Neut_0025"	product="cytochrome c, class I"
complement(21670..24054)	locus_tag="Neut_0026"	product="heavy metal translocating P-type ATPase"
complement(25876..26112)	locus_tag="Neut_0028"	product="mercury resistance protein"
complement(26109..26354)	locus_tag="Neut_0029"	product="MerR family transcriptional regulator"
complement(26372..28075)	locus_tag="Neut_0030"	product="mercuric reductase"
complement(28072..28263)	locus_tag="Neut_0031"	product="hypothetical protein"
complement(28266..28541)	locus_tag="Neut_0032"	product="mercuric transport periplasmic protein"
complement(28557..28907)	locus_tag="Neut_0033"	product="mercuric transport protein"
28979..29455	locus_tag="Neut_0034"	product="transcriptional regulator MerR"
29579..29923	locus_tag="Neut_0035"	product="hypothetical protein"
complement(30220..30732)	locus_tag="Neut_0036"	product="blue (type1) copper domain-containing protein"
complement(31173..32123)	locus_tag="Neut_0037"	product="group 1 glycosyl transferase"
33410..33694	locus_tag="Neut_0038"	product="hypothetical protein"
complement(33837..35171)	locus_tag="Neut_0039"	product="heavy metal sensor signal transduction
complement(35165..35860)	locus_tag="Neut_0040"	product="two component heavy metal response
complement(36163..37185)	locus_tag="Neut_0041"	product="glycosyl transferase"
37709..38254	locus_tag="Neut_0042"	product="hypothetical protein"
complement(38298..39230)	locus_tag="Neut_0043"	product="cation diffusion facilitator family transporter"
39246..39572	locus_tag="Neut_0044"	product="hypothetical protein"
complement(40175..40375)	locus_tag="Neut_0046"	product="hypothetical protein"
complement(40624..40836)	locus_tag="Neut_0047"	product="hypothetical protein"
complement(41297..41983)	locus_tag="Neut_0048"	product="multicopper oxidase, type 2"
complement(42427..44763)	locus_tag="Neut_0049"	product="heavy metal translocating P-type ATPase"

complement(44867..45283)	locus_tag="Neut_0050"	product="hypothetical protein"
complement(45345..45824)	locus_tag="Neut_0051"	product="hypothetical protein"
complement(45875..48139)	locus_tag="Neut_0052"	product="hypothetical protein"
complement(48188..48676)	locus_tag="Neut_0053"	product="hypothetical protein"
complement(48824..49570)	locus_tag="Neut_0054"	product="cytochrome c biogenesis protein, transmembrane
complement(50250..51107)	locus_tag="Neut_0056"	product="hypothetical protein"
complement(51110..51559)	locus_tag="Neut_0057"	product="cytochrome C biogenesis protein"
complement(51556..52080)	locus_tag="Neut_0058"	product="periplasmic protein thiol--disulfide
complement(52077..54038)	locus_tag="Neut_0059"	product="cytochrome c-type biogenesis protein CcmF"
complement(54044..54490)	locus_tag="Neut_0060"	product="CcmE
complement(54666..55403)	locus_tag="Neut_0061"	product="heme exporter protein CcmC"
complement(55415..56098)	locus_tag="Neut_0062"	product="heme exporter protein CcmB"
complement(56095..56709)	locus_tag="Neut_0063"	product="cytochrome c biogenesis protein CcmA"
complement(56916..57272)	locus_tag="Neut_0064"	product="hypothetical protein"
complement(57346..58233)	locus_tag="Neut_0065"	product="methyltransferase type 11"
complement(58277..59326)	locus_tag="Neut_0066"	product="hypothetical protein"
59729..62242	locus_tag="Neut_0067"	product="heavy metal translocating P-type ATPase"
62307..62669	locus_tag="Neut_0068"	product="MerR family transcriptional regulator"
complement(62716..64581)	locus_tag="Neut_0069"	product="relaxase"
64851..65084	locus_tag="Neut_0070"	product="transcriptional regulator
65071..65487	locus_tag="Neut_0071"	product="PilT domain-containing protein"
65510..65875	locus_tag="Neut_0072"	product="hypothetical protein"
complement(65872..67377)	locus_tag="Neut_0073"	product="hypothetical protein"
complement(67393..67737)	locus_tag="Neut_0074"	product="hypothetical protein"
complement(67734..69131)	locus_tag="Neut_0075"	product="hypothetical protein"
complement(69150..70082)	locus_tag="Neut_0076"	product="hypothetical protein"
complement(70079..70510)	locus_tag="Neut_0077"	product="hypothetical protein"
complement(70670..71239)	locus_tag="Neut_0078"	product="hypothetical protein"
complement(71367..71870)	locus_tag="Neut_0079"	product="DNA repair protein RadC"

complement(72068..72820)	locus_tag="Neut_0080"	product="hypothetical protein"
complement(73295..73954)	locus_tag="Neut_0081"	product="DSBA oxidoreductase"
complement(73951..74400)	locus_tag="Neut_0082"	product="disulfide bond formation protein DsbB"
complement(74446..74940)	locus_tag="Neut_0083"	product="hypothetical protein"
complement(75003..77129)	locus_tag="Neut_0084"	product="heavy metal translocating P-type ATPase"
77196..77615	locus_tag="Neut_0085"	product="MerR family transcriptional regulator"
complement(77927..80818)	locus_tag="Neut_0086"	product="hypothetical protein"
complement(80818..81252)	locus_tag="Neut_0087"	product="hypothetical protein"
complement(81233..82630)	locus_tag="Neut_0088"	product="hypothetical protein"
complement(82620..83522)	locus_tag="Neut_0089"	product="hypothetical protein"
complement(83519..84199)	locus_tag="Neut_0090"	product="hypothetical protein"
complement(84196..84594)	locus_tag="Neut_0091"	product="hypothetical protein"
complement(84606..84965)	locus_tag="Neut_0092"	product="hypothetical protein"
complement(84980..85213)	locus_tag="Neut_0093"	product="hypothetical protein"
complement(85210..85581)	locus_tag="Neut_0094"	product="hypothetical protein"
85755..86009	locus_tag="Neut_0095"	product="hypothetical protein"
86137..86865	locus_tag="Neut_0096"	product="hypothetical protein"
complement(86918..87667)	locus_tag="Neut_0097"	product="hypothetical protein"
complement(87664..89838)	locus_tag="Neut_0098"	product="hypothetical protein"
complement(89843..90385)	locus_tag="Neut_0099"	product="hypothetical protein"
complement(90382..90972)	locus_tag="Neut_0100"	product="lytic transglycosylase, catalytic"
complement(90954..91682)	locus_tag="Neut_0101"	product="hypothetical protein"
complement(91697..92347)	locus_tag="Neut_0102"	product="hypothetical protein"
complement(92344..92925)	locus_tag="Neut_0103"	product="hypothetical protein"
complement(93510..95786)	locus_tag="Neut_0104"	product="helicase domain-containing protein"
complement(95890..96201)	locus_tag="Neut_0105"	product="hypothetical protein"
complement(96298..97407)	locus_tag="Neut_0106"	product="hypothetical protein"
complement(97482..98141)	locus_tag="Neut_0107"	product="hypothetical protein"
complement(98306..98647)	locus_tag="Neut_0108"	product="hypothetical protein"

complement(98752..99099)	locus_tag="Neut_0109"	product="plasmid-like protein"TLGCCPAG
complement(99196..99867)	locus_tag="Neut_0110"	product="hypothetical protein"
complement(99975..100889)	locus_tag="Neut_0111"	product="hypothetical protein"
complement(101254..102069)	locus_tag="Neut_0112"	product="hypothetical protein"
complement(102358..103074)	locus_tag="Neut_0113"	product="hypothetical protein"
complement(103275..103838)	locus_tag="Neut_0114"	product="hypothetical protein"
complement(104083..105576)	locus_tag="Neut_0115"	product="DNA-cytosine methyltransferase"
complement(106126..108141)	locus_tag="Neut_0116"	product="DNA topoisomerase III"
complement(108427..108828)	locus_tag="Neut_0117"	product="single-stranded DNA-binding protein"
complement(108886..109413)	locus_tag="Neut_0118"	product="hypothetical protein"
complement(109410..110210)	locus_tag="Neut_0119"	product="hypothetical protein"
complement(110440..111615)	locus_tag="Neut_0120"	product="hypothetical protein"
complement(111619..112179)	locus_tag="Neut_0121"	product="hypothetical protein"
complement(112195..113838)	locus_tag="Neut_0122"	product="hypothetical protein"
complement(113840..114100)	locus_tag="Neut_0123"	product="hypothetical protein"
complement(114093..114953)	locus_tag="Neut_0124"	product="cobyrinic acid a,c-diamide synthase"
complement(114994..115206)	locus_tag="Neut_0125"	product="phage transcriptional regulator AlpA"
complement(115324..116073)	locus_tag="Neut_0126"	product="hypothetical protein"

Table S4: Housekeeping genes used in the phylogenetic analysis.

Gene	Gene product
dnaB	DNA helicase
nusA	transcription elongation factor
pth	peptidyl-tRNA hydrolase
pheS	phenylalanyl-tRNA synthase alpha subunit
obgE	GTP-binding protein
pepA	leucyl aminopeptidase
grpE	heat shock protein
ffh	Signal recognition particle protein
pgk	phosphoglycerate kinase
pyrG	CTP synthase
rplA	50S ribosomal protein
rplB	50S ribosomal protein
rplE	50S ribosomal protein
rplK	50S ribosomal protein
rplO	50S ribosomal protein
rpsB	30S ribosomal protein
rpsE	30S ribosomal protein
rpsG	30S ribosomal protein
rpsH	30S ribosomal protein